

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 18, 2005, 16:18:06 ; Search time 282 Seconds  
(without alignments)  
134.842 Million cell updates/sec

Title: US-09-830-691a-3

Perfect score: 573

Sequence: 1 MNVPTKRTTYCKGKCKKH.....RCKHFELGGDKTKGAISF 106

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_23Sep04:\*

1: Geneseqp1980s:\*

2: Geneseqp1990s:\*

3: Geneseqp2000s:\*

4: Geneseqp2001s:\*

5: Geneseqp2002s:\*

6: Geneseqp2003as:\*

7: Geneseqp2003bs:\*

8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	573	100.0	106	3	AAY94261 Phaffia r
2	495	86.4	106	2	AAR77658 Ribosomal
3	490	85.5	105	7	ADC88814 Ribosomal
4	490	85.5	106	3	AAY55842 P. ciferr
5	483	84.3	106	2	AAY57490 Amino aci
6	483	84.3	106	7	ADC88117 Ribosomal
7	482	84.1	106	4	AAG70870 C albican
8	481	83.9	106	4	AAG70742 S cerevis
9	478	83.4	102	7	ADC88813 Ribosomal
10	478	83.4	116	4	AAG70795 S cerevis
11	476	83.1	105	7	ADC88816 Ribosomal
12	471	82.2	105	7	ADC88805 Ribosomal
13	463	80.8	105	7	ADC88810 Ribosomal
14	462	80.6	106	2	AAR32293 Sequence
15	461	80.5	105	7	ADC88118 Ribosomal
16	460	80.3	105	7	ADC88803 Ribosomal
17	460	80.3	105	7	ADC88024 Ribosomal
18	459	80.1	105	3	AAG22309 Zea mays
19	459	80.1	105	3	AAG19042 Zea mays
20	458	79.9	105	3	AAG33740 Arabidops
21	458	79.9	105	3	AAG37808 Arabidops
22	458	79.9	105	3	AAG10245 Arabidops
23	458	79.9	105	3	AAG45312 Arabidops
24	458	79.9	105	7	ADC88800 Ribosomal
25	458	79.9	105	7	ADE25075 Plant gro

26	458	79.9	122	3	AAG33739 Arabidops
27	457	79.8	105	7	ADC88809 Ribosomal
28	452	78.9	104	7	ADC88806 Ribosomal
29	450	78.5	106	8	ADO57261 Kidney de
30	439.5	76.7	104	7	ADC88802 Ribosomal
31	439	76.6	106	7	ADE59095 Human Pro
32	439	76.6	131	3	AAB43900 Human can
33	436	76.1	106	5	ABP65233 Hypoxia-r
34	436	76.1	137	5	ABP41758 Human ova
35	434	75.7	105	7	ADC88808 Ribosomal
36	434	75.7	105	7	ADE59093 Rat Prote
37	434	75.7	105	7	ADE62528 Human Pro
38	434	75.7	111	5	ABP42647 Human Pro
39	431.5	75.3	105	7	ADC88801 Ribosomal
40	428	74.7	106	5	ABG32266 Human rib
41	428	74.7	106	5	ABG32265 Human rib
42	424	74.0	127	5	ABP64899 Human pro
43	424	74.0	147	4	ABG27187 Novel hum
44	422	73.6	138	4	ABG16314 Novel hum
45	404	70.5	122	4	ABB63267 Drosophill

ALIGNMENTS

RESULT 1  
AAY94261  
ID AAY94261 standard; protein; 106 AA.  
XX  
AC AAY94261;  
XX  
DT 12-SEP-2003 (revised)  
DT 25-SEP-2000 (first entry)  
XX  
DE Phaffia rhodozyma L41.  
XX  
KW Astaxanthin; L41; Yeast; carotenoid; cyclohexamide-resistance;  
KW site-directed mutagenesis; selectable marker; ribosomal protein.  
XX  
OS Xanthophyllomyces dendrothous.  
XX  
PN WO200026387-A1.  
XX  
PD 11-MAY-2000.  
XX  
PF 29-MAY-1999; 99WO-KR000265.  
XX  
PR 31-OCT-1998; 98KR-00046547.  
XX  
(KOAD ) KOREA ADV INST SCI & TECHNOLOGY.  
(HAIT-) HAI TAI CONFECTIONERY CO LTD.

Choi E, Rhee S, Sohn J, Park S, Lee YH, Lee SJ, Jang JK;  
Choi SK, Son YR;

WPI; 2000-365630/31.

N-PSDB; AAA15567, AAA15568.

Novel vector comprising a cyclohexamide-resistance gene and a ribosomal DNA useful for the transformation of Phaffia rhodozyma.

Claim 1; Page 37-38; 43pp; English.

The present sequence is the Phaffia rhodozyma L41 ribosomal protein. The mutated form of the L41 protein, with a glutamine at position 56, instead of a proline (as there is in the wild-type protein) confers cycloheximide resistance on the cell carrying the mutated form of the gene. The mutated form can be produced by site-directed mutagenesis. This antibiotic resistance phenotype can be exploited by using this gene as a selectable marker in a P. rhodozyma vector. The vector can be used to carry foreign DNA, e.g. the astaxanthin gene, a carotenoid. (Updated on 12-SEP-2003 to standardise OS field)

XX

SQ Sequence 106 AA;

Query Match 100.0%; Score 573; DB 3; Length 106;  
 Best Local Similarity 100.0%; Pred. No. 7.2e-61;  
 Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNNVPKTRRTYCKGKACKKHTPHKVTQYKKGKDSIFAQGRYDRKQSGYGQTKPVFHK 60  
 DB 1 MNNVPKTRRTYCKGKACKKHTPHKVTQYKKGKDSIFAQGRYDRKQSGYGQTKPVFHK 60

QY 61 KAKTTKKVLRLECSVKYKQMTLKRCKHFELGGDKTKGAATSF 106  
 DB 61 KAKTTKKVLRLECSVKYKQMTLKRCKHFELGGDKTKGAATSF 106

RESULT 2  
 AAR77658  
 ID AAR77658 standard; protein; 106 AA.  
 XX  
 AC AAR77658;  
 XX  
 DT 16-OCT-2003 (revised)  
 DT 03-DEC-1996 (first entry)  
 XX  
 DB Ribosomal protein L41.  
 XX  
 KW Ribosomal protein; expression vector; heterogene; yeast; GAP; PGK; PMA;  
 KW phosphoglyceric acid kinase; protoplasmic membrane proton ATPase;  
 KW glyceraldehyde-3-phosphoric acid dehydrogenase; resistance marker;  
 KW hygromycin B phosphotransferase; aminoglycoside-3'-phosphotransferase.  
 XX  
 OS Pichia jadinii.  
 XX  
 FN WO9532289-A1.  
 XX  
 PD 30-NOV-1995.  
 XX  
 PF 25-MAY-1995; 95WO-JP001005.  
 XX  
 PR 25-MAY-1994; 94JP-00135015.  
 PR 26-OCT-1994; 94JP-00285823.  
 PR 28-APR-1995; 95JP-00129287.  
 XX  
 PA (KIRI ) KIRIN BEER KK.  
 XX  
 PI Kondo K, Kajiwara S, Misawa N;  
 DR N-PSDB; AAT08602.  
 DR WPI; 1996-020584/02.  
 PT Ribosomal protein L41 gene, promoter and terminator sequences, isolated  
 PT from Candida utilis - used in vector for expression of hetero:gene(s) in  
 PT yeast.  
 XX  
 PS Claim 2; Page 162; 252pp; Japanese.  
 XX  
 CC The L41 ribosomal structural protein gene can be used in the construction  
 CC of expression vectors designed specifically to express heterogenes in  
 CC yeast. The vectors also comprise: a promoter and terminator sequence  
 CC selected from phosphoglyceric acid kinase (PGK), glyceraldehyde-3-  
 CC phosphoric acid dehydrogenase (GAP) and protoplasmic membrane proton  
 CC ATPase (PMA) genes isolated from Candida utilis; a drug resistance marker  
 CC selected from aminoglycoside-3'-phosphotransferase or hygromycin B  
 CC phosphotransferase; and the heterogene to be expressed. L41 confers  
 CC cyclohexamine resistance on the yeast. (Updated on 16-OCT-2003 to  
 CC standardise OS field)  
 XX  
 SQ Sequence 106 AA;

Query Match 86.4%; Score 495; DB 2; Length 106;  
 Best Local Similarity 85.8%; Pred. No. 1.8e-51;  
 Matches 91; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

QY 1 MNNVPKTRRTYCKGKACKKHTPHKVTQYKKGKDSIFAQGRYDRKQSGYGQTKPVFHK 60  
 DB 1 MNNVPKTRRTYCKGKACKKHTPHKVTQYKKGKDSIFAQGRYDRKQSGYGQTKPVFHK 60

QY 61 KAKTTKKVLRLECSVKYKQMTLKRCKHFELGGDKTKGAATSF 106  
 DB 61 KAKTTKKVLRLECSVKYKQMTLKRCKHFELGGDKTKGAATSF 106

RESULT 3  
 ADC88814  
 ID ADC88814 standard; protein; 105 AA.  
 XX  
 AC ADC88814;  
 XX  
 DT 01-JAN-2004 (first entry)  
 XX  
 DE Ribosomal protein similar to FCWP1 #1030.  
 XX  
 KW Antifungal protein; ribosomal protein; FCWP1; AlyAPP;  
 KW plant fungal infection; Alternaria; Ascochyta; Botrytis; Cercospora;  
 KW Colletotrichum; Diplodia; Fusarium; Gaumanomyces; Helminthosporium;  
 KW Macrophomina; Mycosphaerella; Nectria; Peronospora; Phoma;  
 KW Phymatotrichum; Phytophthora; Plasmodia; Podosphaera; Puccinia; Puthium;  
 KW Pyrenophora; Pyricularia; Pythium; Rhizoctonia; Sclerotium; Sclerotinia;  
 KW Septoria; Thielaviopsis; Venturia; Verticillium.  
 OS Unidentified.  
 XX  
 FN US6573361-B1.  
 XX  
 PD 03-JUN-2003.  
 XX  
 PF 07-DEC-2000; 2000US-00732210.  
 XX  
 PR 07-DEC-1999; 99US-0169340P.  
 PR 07-DEC-1999; 99US-0169513P.  
 XX  
 PA (MONS ) MONSANTO TECHNOLOGY LLC.  
 XX  
 PI Bunkers GJ, Liang J, Mittanck CA, Seale JW, Wu YS;  
 DR WPI; 2003-754558/71.  
 XX  
 PT Novel antifungal protein FCWP1, isolated from Fusarium culmorum, useful  
 PT for controlling fungal infections in plants.  
 XX  
 PS Example 21; SEQ ID NO 1067; 27pp; English.  
 XX

The invention relates to an isolated antifungal ribosomal protein from  
 fusarium culmorum, FCWP1. Also included is a fusion protein between the  
 signal peptide of the antifungal protein AlyAPP from Alyssum and FCWP1,  
 encoded by the nucleic acid appearing as ADC87758. The FCWP1 proteins are  
 useful for controlling fungal infections in plants, such as those caused  
 by Alternaria (e.g. Alternaria brassicola, Alternaria solani),  
 Ascochyta (e.g. Ascochyta pisi), Botrytis (e.g. Botrytis cinerea),  
 Cercospora (e.g. Cercospora kikuchii, Cercospora zea-maydis),  
 Colletotrichum (e.g. Colletotrichum lindemuthianum), Diplodia (e.g.  
 Diplodia maydis), Fusarium (e.g. Fusarium nivale, Fusarium oxysporum,  
 Fusarium graminearum, Fusarium culmorum, Fusarium solani, Fusarium  
 moniliforme, Fusarium roseum), Gaumanomyces (e.g. Gaumanomyces  
 graminis f.sp. tritici), Helminthosporium (e.g. Helminthosporium turcicum  
 graminis f.sp. tritici), Helminthosporium maydis), Macrophomina  
 (e.g. Macrophomina phaseolina, Maganaporthe grisea), Mycosphaerella  
 (e.g. Mycosphaerella figiensis), Nectria (Nectria haematococca), Phoma  
 peronospora (e.g. Peronospora manshurica, Peronospora tabacina), Phoma  
 (e.g. Phoma betae), Phymatotrichum (e.g. Phymatotrichum omnivorum),  
 Phytophthora (e.g. Phytophthora cinnamomi, Phytophthora cactorum,  
 Phytophthora phaseoli, Phytophthora parasitica, Phytophthora  
 citrophthora, Phytophthora megasperma f.sp. sojae, Phytophthora  
 infestans), Plasmodia (e.g. Plasmodia viticola), Podosphaera (e.g.  
 Podosphaera leucotricha), Puccinia (e.g. Puccinia sorghi, Puccinia  
 striiformis, Puccinia graminis f.sp. tritici, Puccinia asparagi,

CC Puccinia recondita, Puccinia atachidis, Puthium (e.g. Puthium  
 CC aphanidermatum), Pyrenophora (e.g. Pyrenophora tritici-repentens),  
 CC Pyricularia (e.g. Pyricularia oryzae), Pythium (e.g. Pythium ultimum),  
 CC Rhizoctonia (e.g. Rhizoctonia oryzae), Pythium (e.g. Pythium ultimum),  
 CC Rhizoctonia (e.g. Rhizoctonia solani), Rhizoctonia cerealis, Sclerotium  
 CC (e.g. Sclerotium rolfsii), Sclerotinia (e.g. Sclerotinia sclerotiorum),  
 CC Septoria (e.g. Septoria lycopersici, Septoria glycines, Stagonospora  
 CC nodorum / Phaeosphaeria nodorum, Septoria tritici), Thielaviopsis (e.g.  
 CC Thielaviopsis basicola), Uncinula (e.g. Uncinula necator), Venturia  
 CC (e.g. Venturia inaequalis) or Verticillium (e.g. Verticillium dahliae,  
 CC Verticillium albo-atrum). Mutations in the proteolytic consensus  
 CC sequences contained within FCWP1 provides improved stability of its  
 CC antifungal activity. Also disclosed are ribosomal proteins with similar  
 CC PI (>7) and molecular weight (<20kDa) to FCWP1, which may act as  
 CC antifungal proteins. The present sequence represents one of the ribosomal  
 CC proteins similar to FCWP1. Note: The sequence data for this patent did  
 CC not form part of the printed specification, but was obtained in  
 CC electronic format directly from USPTO at  
 CC seqdata.uspto.gov/sequence.html?DocID=6573361B1.

XX  
 SQ Sequence 105 AA;

Query Match 85.5%; Score 490; DB 7; Length 105;  
 Best Local Similarity 85.7%; Pred. No. 7.2e-51;  
 Matches 90; Conservative 4; Mismatches 11; Indels 0; Gaps 0;  
 Qy 2 VNVPTRTTYCKGKCKKHTPHKVTQYKKGKDSIFAQGRYDRKQSGYGQTKPVFHK 61  
 Db 1 VNVPTRTTYCKGKCKKHTPHKVTQYKKGKASLFAQGRYDRKQSGYGQTKPVFHK 60  
 Qy 62 AKTTKKVLRLECSVCCKYKQMTLKRCKHFGELGDKTKGAATSF 106  
 Db 61 AKTTKKVLRLECVCKTKAQLAKRCKHFGELGDKTKRQQAQLOF 105

RESULT 4  
 AAY55842  
 ID AAY55842 standard; protein; 106 AA.

XX  
 AC AAY55842;  
 DT 06-MAR-2000 (first entry)  
 XX  
 DE P. ciferrii ribosomal protein.

XX L41 gene; ribosomal protein; CYHR gene; cyclohexamide resistance;  
 KW tetraacetyl phytosphingosine; TAPS; ceramide; skin-protection;  
 KW water-loss; skin drying; cosmetic.  
 XX Pichia ciferrii.

XX WO9957279-A1.  
 XX 11-NOV-1999.  
 XX 31-OCT-1998; 98WO-KR000346.  
 XX 07-MAY-1998; 98KR-00016309.  
 XX 07-MAY-1998; 98KR-00016310.  
 XX 21-AUG-1998; 98KR-00033969.  
 XX (DOOSAN CORP.  
 PA (KOAD) KOREA ADV INST SCI & TECHNOLOGY.

XX Rhee SK, Bae JH, Choi ES, Sohn JH, Kang HA, Park CS;  
 XX WPI; 2000-062149/05.  
 DR N-PSDB; AAZ39763.

XX New expression cassettes comprising CYHR gene resistant to cyclohexamide  
 PT and desired gene, used for transforming Pichia ciferrii to produce  
 PT tetraacetyl phytosphingosine.

XX Example 3; Page 50-52; 72pp; English.

XX The invention provides an expression cassette for a desired gene in P.  
 CC ciferrii that comprises: (a) a P. ciferrii ribosomal DNA operably linked  
 CC to; (b) a CYHR gene (L41 gene in which Pro56 is replaced with Glu to give  
 CC cyclohexamide resistance) which is responsible for cyclohexamide,  
 CC operably linked to; and (c) a desired structural gene. The ribosomal L41-  
 CC coding gene was manipulated to give resistance to cyclohexamide, so it  
 CC can be used as a selection marker. The expression cassette is used to  
 CC transform P. ciferrii, especially to produce higher levels of tetraacetyl  
 CC phytosphingosine (TAPS) in a shorter space of time. TAPS is a precursor  
 CC of ceramides, and shows skin-protection activity, and prevents excessive  
 CC water-loss and drying out of the skin, and so is of great use in  
 CC cosmetics. The method is used for producing P. ciferrii mutants which are  
 CC capable of producing higher levels of TAPS than their wild type  
 CC counterparts. The present sequence represents a P. ciferrii ribosomal  
 CC protein encoded by the L41 gene

XX Sequence 106 AA;

Query Match 85.5%; Score 490; DB 3; Length 106;  
 Best Local Similarity 84.0%; Pred. No. 7.3e-51;  
 Matches 89; Conservative 7; Mismatches 10; Indels 0; Gaps 0;  
 Qy 1 MVNVPKTRTYCKGKCKKHTPHKVTQYKKGKDSIFAQGRYDRKQSGYGQTKPVFHK 60  
 Db 1 MVNVPKTRTYCKGKCKKHTPHKVTQYKKGKASLFAQGRYDRKQSGYGQTKPVFHK 60  
 Qy 61 KAKTTKKVLRLECSVCCKYKQMTLKRCKHFGELGDKTKGAATSF 106  
 Db 61 KAKTTKKVLRLECVCKTKAQLAKRCKHFGELGDKTKRQQAQLOF 106

RESULT 5  
 AAW57490  
 ID AAW57490 standard; protein; 106 AA.

XX  
 AC AAW57490;

DT 17-OCT-2003 (revised)  
 DT 14-AUG-1998 (first entry)

DE Amino acid sequence of ragment containing L41 gene.

XX Candida utilis; yeast vector; promoter; marker gene; GAP gene;  
 KW high-efficiency integration; monellin; food; drug; L41; URA3.

OS Pichia jadinii.

XX WO9807873-A1.

XX 26-FEB-1998.

XX 22-AUG-1997; 97WO-JP002924.

XX 23-AUG-1996; 96JP-00241062.

XX (KIRI) KIRIN BEER KK.

XX Kondo K, Miura Y;

XX WPI; 1998-169177/15.

XX N-PSDB; AAV31513.

XX Yeast vector for multi-copying on to chromosomes of yeast such as Candida  
 PT utilis - contains a shortened promoter sequence linked to a marker gene  
 PT for high-efficiency integration.

XX Example; Fig 10; 107pp; Japanese.

XX This is the amino acid sequence of the fragment containing yeast L41  
 CC gene. This can be used in the construction of a yeast vector for multi-  
 CC copying on to chromosomes of yeast such as Candida utilis. The vector  
 CC contains a DNA homologous with a chromosomal gene of the yeast

CC (preferably ribosomal DNA (rDNA) such as the URA3, L41, PGK, GAP or PMA  
 CC gene), a marker gene to be used in transformant selection (such as a drug  
 CC resistance gene, e.g. the cycloheximide resistance gene L41, the G418  
 CC resistance gene Tn903-APT, or the hygromycin B resistance gene (from  
 CC E.coli) HPT), a shortened promoter sequence such as the C-utilis L41,  
 CC phosphoglycerate kinase (PGK), glyceraldehyde-3-phosphate dihydrogenase  
 CC (GAP) or plasma membrane proton ATPase (PMA) gene promoter and a gene of  
 CC interest from yeast or other origin. The vectors are useful in the  
 CC preparation of proteins for food or drug use in high efficiency. They can  
 CC be used especially for the production of single-chain monellin, which is  
 CC a low-calorie sweetener whose thermostability is greater than that of the  
 CC dimeric natural monellin. Multiple copies of the desired gene are  
 CC integrated into the yeast chromosome and high expression efficiency is  
 CC obtained. (Updated on 17-OCT-2003 to standardise OS field)

XX Sequence 106 AA;

Query Match 84.3%; Score 483; DB 2; Length 106;  
 Best Local Similarity 84.0%; Pred. No. 5.1e-50;  
 Matches 89; Conservative 4; Mismatches 13; Indels 0; Gaps 0;

Qy 1 MWNVPTRTTYCKGKCKKHTPHKVTQYKKGKDSIFAQGRYDRKQSGYGQTKPVFHK 60

Db 1 MWNVPTRTTYCKGKCKKHTPHKVTQYKKGKDSIFAQGRYDRKQSGYGQTKPVFHK 60

Qy 61 KAKTTKVVLRLECVCKYKQMTLKRCKHPELGDGDKTKGAALSF 106

Db 61 KAKTTKVVLRLECVCKYKQMTLKRCKHPELGDGDKTKGAALSF 106

#### RESULT 6

ID ADC88117 standard; protein; 106 AA.

AC ADC88117;

DT 01-JAN-2004 (first entry)

DE Ribosomal protein similar to FCWP1 #333.

XX Antifungal protein; ribosomal protein; FCWP1; AlyAPP;  
 KW plant fungal infection; Alternaria; Ascochyta; Botrytis; Cercospora;  
 KW Colletotrichum; Diplodia; Fusarium; Gaemanomyces; Helminthosporium;  
 KW Macrophoma; Mycosphaerella; Nectria; Peronospora; Phoma;  
 KW Phymatotrichum; Phytophthora; Plasmodiopsis; Podosphaera; Puccinia; Puthium;  
 KW Pyrenophora; Pyricularia; Pythium; Rhizoctonia; Sclerotium; Sclerotinia;  
 KW Septoria; Thielaviopsis; Venturia; Verticillium.

XX Unidentified.

XX US6573361-B1.

XX 03-JUN-2003.

XX 07-DEC-2000; 2000US-00732210.

XX 07-DEC-1999; 99US-0169340P.

XX 07-DEC-1999; 99US-0169513P.

XX (MONS ) MONSANTO TECHNOLOGY LLC.

XX Bunkers GJ, Liang J, Mittanck CA, Seale JW, Wu YS;

XX WPI; 2003-754558/71.

XX Novel antifungal protein FCWP1, isolated from Fusarium culmorum, useful  
 PT for controlling fungal infections in plants.

XX Example 21; SEQ ID NO 370; 27pp; English.

XX The invention relates to an isolated antifungal ribosomal protein from  
 CC fusarium culmorum, FCWP1. Also included is a fusion protein between the  
 CC signal peptide of the antifungal protein AlyAPP from Alyseum and FCWP1,

CC encoded by the nucleic acid appearing as ADC87758. The FCWP1 proteins are  
 CC useful for controlling fungal infections in plants, such as those caused  
 CC by Alternaria (e.g. Alternaria brassicola, Alternaria solani),  
 CC Ascochyta (e.g. Ascochyta pisi); Botrytis (e.g. Botrytis cinerea),  
 CC Cercospora (e.g. Cercospora kikuchii, Cercospora zea-maydis),  
 CC Colletotrichum (e.g. Colletotrichum indumethianum), Diplodia (e.g.  
 CC Diplodia maydis), Fusarium (e.g. Fusarium nivale, Fusarium oxysporum,  
 CC Fusarium graminearum, Fusarium culmorum, Fusarium solani, Fusarium  
 CC moniliforme, Fusarium roseum), Gaemanomyces (e.g. Gaemanomyces  
 CC graminis f.sp. tritici), Helminthosporium (e.g. Helminthosporium turcicum  
 CC (e.g. Macrophoma phaseolina, Magnaporthe grisea), Mycosphaerella  
 CC (e.g. Mycosphaerella figiensis), Nectria (Nectria haematococca), Phoma  
 CC (e.g. Phoma betae), Phymatotrichum (e.g. Phymatotrichum omnivorum),  
 CC Phytophthora (e.g. Phytophthora cinnamomi, Phytophthora cactorum,  
 CC Phytophthora phaseoli, Phytophthora parasitica, Phytophthora  
 CC citrophthora, Phytophthora megasperma f.sp. sojae, Phytophthora  
 CC infestans), Plasmodiopsis (e.g. Plasmodiopsis viticola), Podosphaera (e.g.  
 CC Podosphaera leucotricha), Puccinia (e.g. Puccinia sorghi, Puccinia  
 CC striiformis, Puccinia graminis f.sp. tritici, Puccinia asparagi,  
 CC Puccinia recondita, Puccinia arachidis), Puthium (e.g. Puthium  
 CC aphanidermatum), Pyrenophora (e.g. Pyrenophora tritici-repentens),  
 CC Pyricularia (e.g. Pyricularia oryzae), Pythium (e.g. Pythium ultimum),  
 CC Rhizoctonia (e.g. Rhizoctonia solani, Rhizoctonia cerealis), Sclerotium  
 CC (e.g. Sclerotium rolfsii), Sclerotinia (e.g. Sclerotinia sclerotiorum),  
 CC Septoria (e.g. Septoria lycopersici, Septoria glycines, Stagonospora  
 CC nodorum / Phaeosphaeria nodorum, Septoria tritici), Thielaviopsis (e.g.  
 CC Thielaviopsis basicola), Uncinula (e.g. Uncinula necator), Venturia  
 CC (e.g. Venturia inaequalis) or Verticillium (e.g. Verticillium dahliae,  
 CC Verticillium albo-atrum). Mutations in the proteolytic consensus  
 CC sequences contained within FCWP1 provides improved stability of its  
 CC antifungal activity. Also disclosed are ribosomal proteins with similar  
 CC PI (>7) and molecular weight (<20kDa) to FCWP1, which may act as  
 CC antifungal proteins. The present sequence represents one of the ribosomal  
 CC proteins similar to FCWP1. Note: The sequence data for this patent did  
 CC not form part of the printed specification, but was obtained in  
 CC electronic format directly from USPTO at  
 CC seqdata.uspto.gov/sequence.html?DocID=6573361B1.

XX Sequence 106 AA;

Query Match 84.3%; Score 483; DB 7; Length 106;

Best Local Similarity 82.1%; Pred. No. 5.1e-50;

Matches 87; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

Qy 1 MWNVPTRTTYCKGKCKKHTPHKVTQYKKGKDSIFAQGRYDRKQSGYGQTKPVFHK 60

Db 1 MWNVPTRTTYCKGKCKKHTPHKVTQYKKGKDSIFAQGRYDRKQSGYGQTKPVFHK 60

Qy 61 KAKTTKVVLRLECVCKYKQMTLKRCKHPELGDGDKTKGAALSF 106

Db 61 KAKTTKVVLRLECVCKYKQMTLKRCKHPELGDGDKTKGAALSF 106

#### RESULT 7

AAG70870

ID AAG70870 standard; protein; 106 AA.

XX AAG70870;

XX 27-JUL-2001 (first entry)

XX C albicans apoptosis associated protein #50.

XX Yeast; fungus; apoptosis; infection; proliferative disease; vaccine;  
 KW autoimmune disease; ischaemia; neurodegeneration.

XX Candida albicans.

XX WO200102550-A2.

XX 11-JAN-2001.

XX 03-JUL-2000; 2000WO-BE000077.  
 XX 01-JUL-1999; 99EP-00870141.  
 XX (JANC ) JANSSEN PHARM NV.  
 XX Contreras RH, De Backer MD, Luyten WHML, Malcorps IKL;  
 XX Nelissen BJM, Reekmans RJ;  
 XX WPI; 2001-367042/38.  
 XX N-PSDB; AAH29906.  
 XX Yeast and fungal nucleic acids encoding proteins involved in a pathway  
 PT leading to programmed cell death, useful for treating proliferative  
 PT disorders, yeast and fungal infections, or for preventing apoptosis in  
 PT certain diseases.  
 XX Claim 24; Fig 2; 218pp; English.  
 XX The present invention provides the protein and coding sequences of a  
 CC number of apoptosis associated proteins from the yeast *Saccharomyces*  
 CC *cerevisiae* and the fungus *Candida albicans*. These can be used to identify  
 CC treatments for fungal and yeast infections, for proliferative diseases  
 CC and for apoptosis related diseases such as autoimmune diseases, ischaemia  
 CC and neurodegeneration. The present sequence is one of the *C. albicans*  
 CC proteins of the invention  
 XX Sequence 106 AA;  
 XX Query Match 84.1%; Score 482; DB 4; Length 106;  
 XX Best Local Similarity 83.0%; Pred. No. 6.7e-50;  
 XX Matches 88; Conservative 6; Mismatches 12; Indels 0; Gaps 0;  
 QY 1 MNNVPKTRRTYCKGKCKKHTPHKVTQYKKGKDSIFAQGRYDRKOSGYGGQTKPVFHK 60  
 DB 1 MNNVPKTRKTYCKGKCKKHTPHKVTQYKKGKASLFAQGRYDRKOSGYGGQTKPVFHK 60  
 QY 61 KAKTTKKVLRLECSVCKYKMQMTLKRCKHFLGDKKTKGAATSF 106  
 DB 61 KAKTTKKVLRLECSVCKYKMQMTLKRCKHFLGDKKTKGAATSF 106  
 RESULT 8  
 ID AAG70742  
 XX AAG70742 standard; protein; 106 AA.  
 AC AAG70742;  
 XX 27-JUL-2001 (first entry)  
 XX S cerevisiae apoptosis associated protein YHR021C.  
 XX Yeast; fungus; apoptosis; infection; proliferative disease; vaccine;  
 KW autoimmune disease; ischaemia; neurodegeneration.  
 XX Saccharomyces cerevisiae.  
 XX W0200102550-A2.  
 XX 11-JAN-2001.  
 XX 03-JUL-2000; 2000WO-BE000077.  
 XX 01-JUL-1999; 99EP-00870141.  
 XX (JANC ) JANSSEN PHARM NV.  
 XX Contreras RH, De Backer MD, Luyten WHML, Malcorps IKL;  
 XX Nelissen BJM, Reekmans RJ;  
 XX WPI; 2001-367042/38.  
 XX N-PSDB; AAH29778.

XX Yeast and fungal nucleic acids encoding proteins involved in a pathway  
 PT leading to programmed cell death, useful for treating proliferative  
 PT disorders, yeast and fungal infections, or for preventing apoptosis in  
 PT certain diseases.  
 XX Claim 1; Fig 1; 218pp; English.  
 XX The present invention provides the protein and coding sequences of a  
 CC number of apoptosis associated proteins from the yeast *Saccharomyces*  
 CC *cerevisiae* and the fungus *Candida albicans*. These can be used to identify  
 CC treatments for fungal and yeast infections, for proliferative diseases  
 CC and for apoptosis related diseases such as autoimmune diseases, ischaemia  
 CC and neurodegeneration. The present sequence is one of the *S. cerevisiae*  
 CC proteins of the invention  
 XX Sequence 106 AA;  
 XX Query Match 83.9%; Score 481; DB 4; Length 106;  
 XX Best Local Similarity 82.1%; Pred. No. 8.8e-50;  
 XX Matches 87; Conservative 8; Mismatches 11; Indels 0; Gaps 0;  
 QY 1 MNNVPKTRRTYCKGKCKKHTPHKVTQYKKGKDSIFAQGRYDRKOSGYGGQTKPVFHK 60  
 DB 1 MNNVPKTRKTYCKGKCKKHTPHKVTQYKKGKASLFAQGRYDRKOSGYGGQTKPVFHK 60  
 QY 61 KAKTTKKVLRLECSVCKYKMQMTLKRCKHFLGDKKTKGAATSF 106  
 DB 61 KAKTTKKVLRLECSVCKYKMQMTLKRCKHFLGDKKTKGAATSF 106  
 RESULT 9  
 ID ADC88813  
 XX ADC88813 standard; protein; 102 AA.  
 AC ADC88813;  
 XX 01-JAN-2004 (first entry)  
 XX Ribosomal protein similar to FCWP1 #1029.  
 XX Antifungal protein; ribosomal protein; FCWP1; AlyAPP;  
 KW plant fungal infection; Alternaria; Ascochyta; Botrytis; Cercospora;  
 KW Colletotrichum; Diplodia; Fusarium; Gaeumannomyces; Helminthosporium;  
 KW Macrophomina; Mycosphaerella; Nectria; Peronospora; Phoma;  
 KW Phymatotrichum; Phytophthora; Plasmodiopsis; Podosphaera; Puccinia; Puthium;  
 KW Pyrenophora; Pyricularia; Pythium; Rhizoctonia; Sclerotium; Sclerotinia;  
 KW Septoria; Thielaviopsis; Venturia; Verticillium.  
 XX Unidentified.  
 XX US6573361-B1.  
 XX 03-JUN-2003.  
 XX 07-DEC-2000; 2000US-00732210.  
 XX 07-DEC-1999; 99US-0169340P.  
 XX 07-DEC-1999; 99US-0169513P.  
 XX (MONS ) MONSANTO TECHNOLOGY LLC.  
 XX Bunkers GJ, Liang J, Mittanck CA, Seale JW, Wu YS;  
 XX WPI; 2003-754558/71.  
 XX Novel antifungal protein FCWP1, isolated from *Fusarium culmorum*, useful  
 PT for controlling fungal infections in plants.  
 XX Example 21; SEQ ID NO 1066; 27pp; English.  
 XX The invention relates to an isolated antifungal ribosomal protein from the  
 CC *Fusarium culmorum*, FCWP1. Also included is a fusion protein between the

CC signal peptide of the antifungal protein AlyAPP from *Alyssum* and FCWP1,  
 CC encoded by the nucleic acid appearing as ADC87758. The FCWP1 proteins are  
 CC useful for controlling fungal infections in plants, such as those caused  
 CC by *Alternaria* (e.g. *Alternaria brassicicola*, *Alternaria solani*),  
 CC *Ascochyta* (e.g. *Ascochyta pisi*), *Botrytis* (e.g. *Botrytis cinerea*),  
 CC *Cercospora* (e.g. *Cercospora kikuchii*, *Cercospora zaeae-maydis*),  
 CC *Colletotrichum* (e.g. *Colletotrichum lindemuthianum*), *Diplodia* (e.g.  
 CC *Diplodia maydis*), *Fusarium* (e.g. *Fusarium nivale*, *Fusarium oxysporum*,  
 CC *Fusarium graminearum*, *Fusarium culmorum*, *Fusarium solani*, *Fusarium*  
 CC *moniliforme*, *Fusarium roseum*), *Gaeumannomyces* (e.g. *Gaeumannomyces*  
 CC *graminis* f.sp. *tritici*), *Helminthosporium* (e.g. *Helminthosporium turcicum*  
 CC *graminis* f.sp. *tritici*), *Helminthosporium maydis*), *Macrophomina*  
 CC (e.g. *Macrophomina phaseolina*, *Magnaporthe grisea*), *Mycosphaerella*  
 CC (e.g. *Mycosphaerella figiensis*), *Nectria* (e.g. *Nectria haematococca*), *Phoma*  
 CC *peronospora* (e.g. *Peronospora manshurica*, *Peronospora tabacina*), *Phoma*  
 CC (e.g. *Phoma betae*), *Phymatotrichum* (e.g. *Phymatotrichum omnivorum*),  
 CC *Phytophthora* (e.g. *Phytophthora cinnamomi*, *Phytophthora cactorum*,  
 CC *Phytophthora phaseoli*, *Phytophthora parasitica*, *Phytophthora*  
 CC *citrophthora*, *Phytophthora megasperma* f.sp. *sojae*, *Phytophthora*  
 CC *infestans*), *Plasmopara* (e.g. *Plasmopara viticola*), *Podosphaera* (e.g.  
 CC *Podosphaera leucotricha*), *Puccinia* (e.g. *Puccinia sorghi*, *Puccinia*  
 CC *striformis*, *Puccinia graminis* f.sp. *tritici*, *Puccinia asparagi*,  
 CC *Puccinia recondita*, *Puccinia arachidis*), *Puthium* (e.g. *Puthium*  
 CC *aphanidermatum*), *Pyrenophora* (e.g. *Pyrenophora tritici-repentens*),  
 CC *Pycularia* (e.g. *Pycularia oryzae*), *Pythium* (e.g. *Pythium ultimum*),  
 CC *Rhizoctonia* (e.g. *Rhizoctonia solani*, *Rhizoctonia cerealis*), *Sclerotium*  
 CC (e.g. *Sclerotium rolfsii*), *Sclerotinia* (e.g. *Sclerotinia sclerotiorum*),  
 CC *Septoria* (e.g. *Septoria lycopersici*, *Septoria glycines*, *Stragonospora*  
 CC *nodorum* / *Phaeosphaeria nodorum*, *Septoria tritici*), *Thielaviopsis* (e.g.  
 CC *Thielaviopsis basicola*), *Uncinula* (e.g. *Uncinula necator*), *Venturia*  
 CC (e.g. *Venturia inaequalis*) or *Verticillium* (e.g. *Verticillium dahliae*,  
 CC *Verticillium albo-atrum*). Mutations in the proteolytic consensus  
 CC sequences contained within FCWP1 provides improved stability of its  
 CC antifungal activity. Also disclosed are ribosomal proteins with similar  
 CC PI (>7) and molecular weight (<20kDa) to FCWP1, which may act as  
 CC antifungal proteins. The present sequence represents one of the ribosomal  
 CC proteins similar to FCWP1. Note: The sequence data for this patent did  
 CC not form part of the printed specification, but was obtained in  
 CC electronic format directly from USPTO at  
 CC seqdata.uspto.gov/sequence.html?DocID=6573361B1.

XX Sequence 102 AA;

Query Match 83.4%; Score 478; DB 7; Length 102;  
 Best Local Similarity 86.3%; Pred. No. 1.9e-49;  
 Matches 88; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 2 VNVPKTRTYCKGKACKKHTPHKVTQYKKGKDSIFAQGRYDRKQSGYGQTKPVFHK 61

Db 1 VNVPKTRTYCKGKDCRKHHTQHKVTQYKAGKASLFAQGRYDRKQSGYGQTKPVFHK 60

QY 62 AKTTKKVVLRLCSVCVKYKQMTLKRCKHFELGGDKTKGAA 103

Db 61 AKTTKKVVLRLCSVCVKYKQMTLKRCKHFELGGDKTKGAA 102

RESULT 10

AAG70795

ID AAG70795 standard; protein; 116 AA.

XX AC AAG70795;

XX 27-JUL-2001 (first entry)

XX S cerevisiae apoptosis associated protein YNL096C.

XX Yeast; fungus; apoptosis; infection; proliferative disease; vaccine;

XX autoimmune disease; ischaemia; neurodegeneration.

XX Saccharomyces cerevisiae.

XX WO200102550-A2.

XX

PD 11-JAN-2001.

XX 03-JUL-2000; 2000WO-BE000077.

XX 01-JUL-1999; 99EP-00870141.

XX (JANC ) JANSSEN PHARM NV.

XX Contreras RH, De Backer MD, Luyten WHML, Malcorps IKL;

PI Nelissen BJM, Reekmans RJ;

XX WPI; 2001-367042/38.

DR N-PSDB; AAH29831.

XX Yeast and fungal nucleic acids encoding proteins involved in a pathway  
 PT leading to programmed cell death, useful for treating proliferative  
 PT disorders, yeast and fungal infections, or for preventing apoptosis in  
 PT certain diseases.

XX Claim 1; Fig 1; 218pp; English.

XX The present invention provides the protein and coding sequences of a  
 CC number of apoptosis associated proteins from the yeast *Saccharomyces*  
 CC *cerevisiae* and the fungus *Candida albicans*. These can be used to identify  
 CC treatments for fungal and yeast infections, for proliferative diseases  
 CC and for apoptosis related diseases such as autoimmune diseases, ischaemia  
 CC and neurodegeneration. The present sequence is one of the *S. cerevisiae*  
 CC proteins of the invention

XX Sequence 116 AA;

Query Match 83.4%; Score 478; DB 4; Length 116;  
 Best Local Similarity 81.1%; Pred. No. 2.3e-49;  
 Matches 86; Conservative 9; Mismatches 11; Indels 0; Gaps 0;

QY 1 MNVPKTRTYCKGKACKKHTPHKVTQYKKGKDSIFAQGRYDRKQSGYGQTKPVFHK 60

Db 11 LVNVPKTRTYCKGKTCRKHHTQHKVTQYKAGKASLFAQGRYDRKQSGYGQTKPVFHK 70

QY 61 KAKTTKKVVLRLCSVCVKYKQMTLKRCKHFELGGDKTKGAAISF 106

Db 71 KAKTTKKVVLRLCSVCVKYKQMTLKRCKHFELGGDKTKGAAISF 116

RESULT 11

ADC88816

ID ADC88816 standard; protein; 105 AA.

XX AC ADC88816;

XX 01-JAN-2004 (first entry)

XX Ribosomal protein similar to FCWP1 #1032.

XX Antifungal protein; ribosomal protein; FCWP1; AlyAPP;

XX plant fungal infection; *Alternaria*; *Ascochyta*; *Botrytis*; *Cercospora*;

XX *Colletotrichum*; *Diplodia*; *Fusarium*; *Gaeumannomyces*; *Helminthosporium*;

XX *Macrophomina*; *Mycosphaerella*; *Nectria*; *Peronospora*; *Phoma*;

XX *Phymatotrichum*; *Phytophthora*; *Plasmopara*; *Podosphaera*; *Puccinia*; *Puthium*;

XX *Pyrenophora*; *Pycularia*; *Pythium*; *Rhizoctonia*; *Sclerotium*; *Sclerotinia*;

XX *Septoria*; *Thielaviopsis*; *Venturia*; *Verticillium*.

XX Unidentified.

XX US6573361-B1.

XX 03-JUN-2003.

XX 07-DEC-2000; 2000US-00732210.

XX 07-DEC-1999; 99US-0169340P.

XX 07-DEC-1999; 99US-0169513P.

XX

PA (MONS ) MONSANTO TECHNOLOGY LLC.  
 XX Bunkers GJ, Liang J, Mittanck CA, Seale JW, Wu YS;  
 PI WPI; 2003-754558/71.  
 XX  
 XX  
 XX Novel antifungal protein FCWP1, isolated from *Fusarium culmorum*, useful  
 PT for controlling fungal infections in plants.  
 XX  
 XX Example 21; SEQ ID NO 1069; 27pp; English.  
 XX  
 XX The invention relates to an isolated antifungal ribosomal protein from  
 CC *Fusarium culmorum*, FCWP1. Also included is a fusion protein between the  
 CC signal peptide of the antifungal protein AlyAPP from *Alyseum* and FCWP1,  
 CC encoded by the nucleic acid appearing as ADC8758. The FCWP1 proteins are  
 CC useful for controlling fungal infections in plants, such as those caused  
 CC by *Alternaria* (e.g. *Alternaria brassicola*, *Alternaria solani*),  
 CC *Ascochyta* (e.g. *Ascochyta pisi*); *Botrytis* (e.g. *Botrytis cinerea*),  
 CC *Cercospora* (e.g. *Cercospora kikuchii*, *Cercospora zea-maydis*),  
 CC *Colletotrichum* (e.g. *Colletotrichum lindemuthianum*), *Diplodia* (e.g.  
 CC *Diplodia maydis*), *Fusarium* (e.g. *Fusarium nivale*, *Fusarium oxysporum*,  
 CC *Fusarium graminearum*, *Fusarium roseum*), *Gaeumannomyces* (e.g. *Gaeumannomyces*  
 CC *graminis f. sp. tritici*), *Helminthosporium* (e.g. *Helminthosporium turcicum*  
 CC *graminis f. sp. tritici*), *Helminthosporium maydis*), *Macrophomina*  
 CC (e.g. *Macrophomina phaseolina*, *Maganaporthe grisea*), *Mycosphaerella*  
 CC (e.g. *Mycosphaerella figiensis*), *Nectria* (e.g. *Nectria haematococca*),  
 CC *Peronospora* (e.g. *Peronospora manshurica*, *Peronospora tabacina*), *Phoma*  
 CC (e.g. *Phoma betae*), *Phymatotrichum* (e.g. *Phymatotrichum omnivorum*),  
 CC *Phytophthora* (e.g. *Phytophthora cinnamomi*, *Phytophthora cactorum*,  
 CC *Phytophthora phaseoli*, *Phytophthora parasitica*, *Phytophthora*  
 CC *citrophthora*, *Phytophthora megasperma f. sp. sojae*, *Phytophthora*  
 CC *infestans*), *Plasmopara* (e.g. *Plasmopara viticola*), *Podosphaera* (e.g.  
 CC *Podosphaera leucotricha*), *Puccinia* (e.g. *Puccinia sorghi*, *Puccinia*  
 CC *striformis*, *Puccinia graminis f. sp. tritici*, *Puccinia asparagi*,  
 CC *Puccinia recondita*, *Puccinia arachidis*), *Puthium* (e.g. *Puthium*  
 CC *aphanidermatum*), *Pyrenophora* (e.g. *Pyrenophora tritici-repentens*),  
 CC *Rhizoctonia* (e.g. *Rhizoctonia oryzae*), *Pythium* (e.g. *Pythium ultimum*),  
 CC *Rhizoctonia* (e.g. *Rhizoctonia solani*, *Rhizoctonia cerealis*), *Sclerotium*  
 CC (e.g. *Sclerotium rolfsii*), *Sclerotinia* (e.g. *Sclerotinia sclerotiorum*),  
 CC *Septoria* (e.g. *Septoria lycopersici*, *Septoria glycines*, *Stagonospora*  
 CC *nodorum* / *Phaeosphaeria nodorum*, *Septoria tritici*), *Thielaviopsis* (e.g.  
 CC *Thielaviopsis basicola*), *Uncinula* (e.g. *Uncinula necator*), *Venturia*  
 CC (e.g. *Venturia inaequalis*) or *Verticillium* (e.g. *Verticillium dahliae*,  
 CC *Verticillium albo-atrum*). Mutations in the proteolytic consensus  
 CC sequences contained within FCWP1 provides improved stability of its  
 CC antifungal activity. Also disclosed are ribosomal proteins with similar  
 CC PI (>7) and molecular weight (<20kDa) to FCWP1, which may act as  
 CC antifungal proteins. The present sequence represents one of the ribosomal  
 CC proteins similar to FCWP1. Note: The sequence data for this patent did  
 CC not form part of the printed specification, but was obtained in  
 CC electronic format directly from USPTO at  
 CC seqdata.uspto.gov/sequence.html?docID=6573361B1.  
 XX  
 XX Sequence 105 AA;  
 Sg  
 Query Match 83.1%; Score 476; DB 7; Length 105;  
 Best Local Similarity 81.9%; Pred. No. 3.5e-49;  
 Matches 86; Conservative 8; Mismatches 11; Indels 0; Gaps 0;  
 Qy 2 VNVPKTRTYCKGKCKKTHPKVQYKKGKDSIFAGKRRYDRKQSGYGQTKPVFHK 61  
 Db 1 VNVPKTRTYCKGKCKKTHPKVQYKKGKDSIFAGKRRYDRKQSGYGQTKPVFHK 60  
 Qy 62 AKTKKKVLECSVKCKQMTLKRCKHPELGDKTKGAATSF 106  
 Db 61 AKTKKKVLECSVKCKQMTLKRCKHPELGDKTKGAATSF 105  
 RESULT 12  
 ADC88805  
 ID ADC88805 standard; protein; 105 AA.  
 XX

AC ADC88805;  
 XX  
 XX 01-JAN-2004 (first entry)  
 XX  
 XX Ribosomal protein similar to FCWP1 #1021.  
 XX  
 XX Antifungal protein; ribosomal protein; FCWP1; AlyAPP;  
 KW plant fungal infection; *Alternaria*; *Ascochyta*; *Botrytis*; *Cercospora*;  
 KW *Colletotrichum*; *Diplodia*; *Fusarium*; *Gaeumannomyces*; *Helminthosporium*;  
 KW *Macrophomina*; *Mycosphaerella*; *Nectria*; *Peronospora*; *Phoma*;  
 KW *Phymatotrichum*; *Phytophthora*; *Plasmopara*; *Podosphaera*; *Puccinia*; *Puthium*;  
 KW *Pyrenophora*; *Pycularia*; *Pythium*; *Rhizoctonia*; *Sclerotium*; *Sclerotinia*;  
 KW *Septoria*; *Thielaviopsis*; *Venturia*; *Verticillium*.  
 XX  
 XX Unidentified.  
 OS  
 XX US6573361-B1.  
 XX  
 XX 03-JUN-2003.  
 PD  
 XX 07-DEC-2000; 2000US-00732210.  
 XX  
 XX 07-DEC-1999; 99US-0169340P.  
 PF  
 XX 07-DEC-1999; 99US-0169513P.  
 PR  
 XX (MONS ) MONSANTO TECHNOLOGY LLC.  
 PA  
 XX Bunkers GJ, Liang J, Mittanck CA, Seale JW, Wu YS;  
 PI WPI; 2003-754558/71.  
 XX  
 XX Novel antifungal protein FCWP1, isolated from *Fusarium culmorum*, useful  
 PT for controlling fungal infections in plants.  
 XX  
 XX Example 21; SEQ ID NO 1058; 27pp; English.  
 PS  
 XX The invention relates to an isolated antifungal ribosomal protein from  
 CC *Fusarium culmorum*, FCWP1. Also included is a fusion protein between the  
 CC signal peptide of the antifungal protein AlyAPP from *Alyseum* and FCWP1,  
 CC encoded by the nucleic acid appearing as ADC8758. The FCWP1 proteins are  
 CC useful for controlling fungal infections in plants, such as those caused  
 CC by *Alternaria* (e.g. *Alternaria brassicola*, *Alternaria solani*),  
 CC *Ascochyta* (e.g. *Ascochyta pisi*); *Botrytis* (e.g. *Botrytis cinerea*),  
 CC *Cercospora* (e.g. *Cercospora kikuchii*, *Cercospora zea-maydis*),  
 CC *Colletotrichum* (e.g. *Colletotrichum lindemuthianum*), *Diplodia* (e.g.  
 CC *Diplodia maydis*), *Fusarium* (e.g. *Fusarium nivale*, *Fusarium oxysporum*,  
 CC *Fusarium graminearum*, *Fusarium roseum*), *Gaeumannomyces* (e.g. *Gaeumannomyces*  
 CC *graminis f. sp. tritici*), *Helminthosporium* (e.g. *Helminthosporium turcicum*  
 CC *graminis f. sp. tritici*), *Helminthosporium maydis*), *Macrophomina*  
 CC (e.g. *Macrophomina phaseolina*, *Maganaporthe grisea*), *Mycosphaerella*  
 CC (e.g. *Mycosphaerella figiensis*), *Nectria* (e.g. *Nectria haematococca*),  
 CC *Peronospora* (e.g. *Peronospora manshurica*, *Peronospora tabacina*), *Phoma*  
 CC (e.g. *Phoma betae*), *Phymatotrichum* (e.g. *Phymatotrichum omnivorum*),  
 CC *Phytophthora* (e.g. *Phytophthora cinnamomi*, *Phytophthora cactorum*,  
 CC *Phytophthora phaseoli*, *Phytophthora parasitica*, *Phytophthora*  
 CC *citrophthora*, *Phytophthora megasperma f. sp. sojae*, *Phytophthora*  
 CC *infestans*), *Plasmopara* (e.g. *Plasmopara viticola*), *Podosphaera* (e.g.  
 CC *Podosphaera leucotricha*), *Puccinia* (e.g. *Puccinia sorghi*, *Puccinia*  
 CC *striformis*, *Puccinia graminis f. sp. tritici*, *Puccinia asparagi*,  
 CC *Puccinia recondita*, *Puccinia arachidis*), *Puthium* (e.g. *Puthium*  
 CC *aphanidermatum*), *Pyrenophora* (e.g. *Pyrenophora tritici-repentens*),  
 CC *Rhizoctonia* (e.g. *Rhizoctonia oryzae*), *Pythium* (e.g. *Pythium ultimum*),  
 CC *Rhizoctonia* (e.g. *Rhizoctonia solani*, *Rhizoctonia cerealis*), *Sclerotium*  
 CC (e.g. *Sclerotium rolfsii*), *Sclerotinia* (e.g. *Sclerotinia sclerotiorum*),  
 CC *Septoria* (e.g. *Septoria lycopersici*, *Septoria glycines*, *Stagonospora*  
 CC *nodorum* / *Phaeosphaeria nodorum*, *Septoria tritici*), *Thielaviopsis* (e.g.  
 CC *Thielaviopsis basicola*), *Uncinula* (e.g. *Uncinula necator*), *Venturia*  
 CC (e.g. *Venturia inaequalis*) or *Verticillium* (e.g. *Verticillium dahliae*,  
 CC *Verticillium albo-atrum*). Mutations in the proteolytic consensus  
 CC sequences contained within FCWP1 provides improved stability of its  
 CC antifungal activity. Also disclosed are ribosomal proteins with similar  
 CC PI (>7) and molecular weight (<20kDa) to FCWP1, which may act as  
 CC antifungal proteins. The present sequence represents one of the ribosomal  
 CC proteins similar to FCWP1. Note: The sequence data for this patent did  
 CC not form part of the printed specification, but was obtained in  
 CC electronic format directly from USPTO at  
 CC seqdata.uspto.gov/sequence.html?docID=6573361B1.  
 XX



CC antifungal proteins. The present sequence represents one of the ribosomal  
 CC proteins similar to FCWP1. Note: The sequence data for this patent did  
 CC not form part of the printed specification, but was obtained in  
 CC electronic format directly from USPTO at  
 CC seqdata.uspto.gov/sequence.html?DocID=6573361B1.

XX SQ Sequence 105 AA;

Query Match 82.2%; Score 471; DB 7; Length 105;  
 Best Local Similarity 81.0%; Pred. No. 1.4e-48;  
 Matches 85; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

QY 2 VNVPKTRTYCKGKACKKHPPHKVQYKKGKDSIFAQGRYDRKQSGYGGQTKPVPHKK 61

Db 1 VNVPKTRTYCKGKACKKHPPHKVQYKKGKDSIFAQGRYDRKQSGYGGQTKPVPHKK 60

QY 62 AKTTKKVLLRLECSVCYKQMTLKRCKHFLGDKTKTGAATSF 106

Db 61 AKTTKKVLLRLECSVCYKQMTLKRCKHFLGDKTKTGAATSF 105

#### RESULT 13

ADC88810  
 ID ADC88810 standard; protein; 105 AA.

XX AC ADC88810;

XX DT 01-JAN-2004 (first entry)

XX DE Ribosomal protein similar to FCWP1 #1026.

XX KW Antifungal protein; ribosomal protein; FCWP1; AlyAPP;

XX KW plant fungal infection; Alternaria; Ascochyta; Botrytis; Cercospora;

XX KW Colletotrichum; Diplodia; Fusarium; Gaeumannomyces; Helminthosporium;

XX KW Macrophoma; Mycosphaerella; Nectria; Peronospora; Phoma;

XX KW Phymatotrichum; Phytophthora; Plasmopara; Podosphaera; Puccinia; Puthium;

XX KW Pyrenophora; Pyricularia; Pythium; Rhizoctonia; Sclerotium; Sclerotinia;

XX KW Septoria; Thielaviopsis; Venturia; Verticillium.

XX OS Unidentified.

XX FN US6573361-B1.

XX PD 03-JUN-2003.

XX PF 07-DEC-2000; 2000US-00732210.

XX PR 07-DEC-1999; 99US-0169340P.

XX PR 07-DEC-1999; 99US-0169513P.

XX PA (MONS) MONSANTO TECHNOLOGY LLC.

XX PI Bunkers GJ, Liang J, Mittanck CA, Seale JW, Wu YS;

XX DR WPI; 2003-754558/71.

XX PT Novel antifungal protein FCWP1, isolated from Fusarium culmorum, useful  
 XX for controlling fungal infections in plants.

XX FS Example 21; SEQ ID NO 1063; 27pp; English.

XX The invention relates to an isolated antifungal ribosomal protein from  
 CC fusarium culmorum, FCWP1. Also included is a fusion protein between the  
 CC signal peptide of the antifungal protein AlyAPP from Alyssum and FCWP1,  
 CC encoded by the nucleic acid appearing as ADC87758. The FCWP1 proteins are  
 CC useful for controlling fungal infections in plants, such as those caused  
 CC by Alternaria (e.g. Alternaria brassicicola, Alternaria solani),  
 CC Ascochyta (e.g. Ascochyta pisi); Botrytis (e.g. Botrytis cinerea),  
 CC Cercospora (e.g. Cercospora kikuchii, Cercospora zea-maydis),  
 CC Colletotrichum (e.g. Colletotrichum lindemuthianum), Diplodia (e.g.  
 CC Diplodia maydis), Fusarium (e.g. Fusarium nivale, Fusarium oxysporum,  
 CC Fusarium graminearum, Fusarium culmorum, Fusarium solani, Fusarium  
 CC moniliforme, Fusarium roseum), Gaeumannomyces (e.g. Gaeumannomyces

CC graminis f.sp. tritici), Helminthosporium (e.g. Helminthosporium turcicum  
 CC Helminthosporium carbonum, Helminthosporium maydis), Macrophoma  
 CC (e.g. Macrophoma phaseolina, Maganaporthe grisea), Mycosphaerella  
 CC (e.g. Mycosphaerella figiensis), Nectria (Nectria heamatococca), Phoma  
 CC Peronospora (e.g. Peronospora manshurica, Peronospora tabacina), Phoma  
 CC (e.g. Phoma betae), Phymatotrichum (e.g. Phymatotrichum omnivorum),  
 CC Phytophthora (e.g. Phytophthora cinnamomi, Phytophthora cactorum,  
 CC Phytophthora phaseoli, Phytophthora parasitica, Phytophthora  
 CC citrophthora, Phytophthora megasperma f.sp. sojae, Phytophthora  
 CC infestans), Plasmopara (e.g. Plasmopara viticola), Podosphaera (e.g.  
 CC Podosphaera leucotricha), Puccinia (e.g. Puccinia sorghi, Puccinia  
 CC striformis, Puccinia graminis f.sp. tritici, Puccinia asparagi,  
 CC Puccinia recondita, Puccinia arachidis), Puthium (e.g. Puthium  
 CC aphanidermatum), Pyrenophora (e.g. Pyrenophora tritici-repentens),  
 CC Pyricularia (e.g. Pyricularia oryzae), Pythium (e.g. Pythium ultimum),  
 CC Rhizoctonia (e.g. Rhizoctonia solani, Rhizoctonia cerealis), Sclerotium  
 CC (e.g. Sclerotium rolfsii), Sclerotinia (e.g. Sclerotinia sclerotiorum),  
 CC Septoria (e.g. Septoria lycopersici, Septoria tritici), Stagonospora  
 CC nodorum / Phaeosphaeria nodorum, Septoria tritici, Thielaviopsis  
 CC Thielaviopsis basicola), Uncinula (e.g. Uncinula necator), Venturia  
 CC Verticillium albo-atrum). Mutations in the proteolytic consensus  
 CC sequences contained within FCWP1 provides improved stability of its  
 CC antifungal activity. Also disclosed are ribosomal proteins with similar  
 CC antifungal proteins. The present sequence represents one of the ribosomal  
 CC proteins similar to FCWP1. Note: The sequence data for this patent did  
 CC not form part of the printed specification, but was obtained in  
 CC electronic format directly from USPTO at  
 CC seqdata.uspto.gov/sequence.html?DocID=6573361B1.

XX SQ Sequence 105 AA;

Query Match 80.8%; Score 463; DB 7; Length 105;

Best Local Similarity 79.0%; Pred. No. 1.3e-47;

Matches 83; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

QY 2 VNVPKTRTYCKGKACKKHPPHKVQYKKGKDSIFAQGRYDRKQSGYGGQTKPVPHKK 61

Db 1 VNVPKTRTYCKGKACKKHPPHKVQYKKGKDSIFAQGRYDRKQSGYGGQTKPVPHKK 60

QY 62 AKTTKKVLLRLECSVCYKQMTLKRCKHFLGDKTKTGAATSF 106

Db 61 AKTTKKVLLRLECSVCYKQMTLKRCKHFLGDKTKTGAATSF 105

#### RESULT 14

AAR32293  
 ID AAR32293 standard; protein; 106 AA.

XX AC AAR32293;

XX DT 25-MAR-2003 (revised)

XX DT 08-JUN-1993 (first entry)

XX DE Sequence of ribosomal resistance protein A which confers resistant to  
 XX cycloheximide.

XX KW Cycloheximide resistance protein; protein A; ribosomal protein.

XX OS Kluyveromyces lactis.

XX FN W09302201-A1.

XX PD 04-FEB-1993.

XX PF 15-JUL-1992; 92WO-FR000685.

XX PR 15-JUL-1991; 91FR-00008906.

XX PA (INSP) INST PASTEUR.

XX PI Dehoux P, Davies J;



XX	WPI; 1993-058797/07.
XX	
XX	New nucleic acid fragment imparting resistance to cycloheximide -
XX	isolated from Kluyveromyces lactis, useful as selection marker for DNA
XX	transfer in eukaryotic cells.
XX	
XX	Claim 11; Fig 4; 42pp; French.
XX	
XX	DNA sequence I encodes a 106 AA ribosomal resistance protein. It is
XX	derived from Kluyveromyces lactis. The protein confers resistance to
XX	cycloheximide (Ch) at over 1ng/ml in both K. lactis and Saccharomyces
XX	cerevisiae. DNA sequence II encodes the resistance protein and a
XX	cofactor. The open reading frame of DNA sequence II extends from bases 1-
XX	1560; it contains 2 exons 629-632 and 1223-1539 and includes the gene
XX	promoter. The co-factor is encoded by region 1561-2740. Cells transformed
XX	with the nucleic acid sequences become resistant to Ch and so the
XX	sequences can be used as a selection marker for controlling the transfer
XX	of nucleic acid. (Updated on 25-MAR-2003 to correct PN field.)
XX	
XX	Sequence 106 AA;
XX	
XX	Query Match 80.6%; Score 462; DB 2; Length 106;
XX	Best Local Similarity 78.3%; Pred.No. 1.7e-47;
XX	Matches 83; Conservative 9; Mismatches 14; Indels 0; Gaps 0;
XX	
QY	1 MNNVPTKRTYCKGKACKHTPHKVTQYKKGKDSIFAQKKRRYDRKQSGYGQTKPVFHK 60
DB	1 MNNVPTKRTYCKGKCKEKAQHKVTQYKAGKASLYAQKKRRYDRKQSGFGQTKQIFHK 60
QY	61 KATTKKKVLRLEGSCVKYKQMTLKRCKHFELGGDKTKGAATSP 106
DB	61 KATTKKKVLRLEGSCVKTKTQLALKRCKHFELGGEKKQKQALQF 106
XX	
XX	RESULT 15
XX	ADC88118
XX	ID ADC88118 standard; protein; 105 AA.
XX	ID ADC88118;
XX	DT 01-JAN-2004 (first entry)
XX	XX Ribosomal protein similar to FCWP1 #334.
XX	XX Antifungal protein; ribosomal protein; FCWP1; AlyAFP;
XX	XX plant fungal infection; Alternaria; Ascochyta; Botrytis; Cercospora;
XX	XX Colletotrichum; Diplodia; Fusarium; Gaeumannomyces; Helminthosporium;
XX	XX Macrophomina; Mycosphaerella; Nectria; Peronospora; Phoma;
XX	XX Phymatotrichum; Phytophthora; Plasmodiopsis; Podosphaera; Puccinia; Puthium;
XX	XX Pyrenophora; Pyricularia; Pythium; Rhizoctonia; Sclerotium; Sclerotinia;
XX	XX Septoria; Thielaviopsis; Venturia; Verticillium.
XX	XX Unidentified.
XX	XX OS
XX	XX US6573361-B1.
XX	XX PN
XX	XX PD 03-JUN-2003.
XX	XX 07-DEC-2000; 2000US-00732210.
XX	XX 07-DEC-1999; 99US-0169340P.
XX	XX PR 07-DEC-1999; 99US-0169513P.
XX	XX (MONS ) MONSANTO TECHNOLOGY LLC.
XX	XX PA
XX	XX Bunkers GJ, Liang J, Mittanck CA, Seale JW, Wu YS;
XX	XX WPI; 2003-754558/71.
XX	
XX	Novel antifungal protein FCWP1, isolated from Fusarium culmorum, useful
XX	for controlling fungal infections in plants.
XX	
XX	

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OM nucleic - nucleic search, using sw model

Run on: January 18, 2005, 08:40:39 ; Search time 448.315 Seconds  
(without alignments)  
8676.543 Million cell updates/sec

Title: US-09-830-691A-4  
Perfect score: 741  
Sequence: 1 ctgagtggcgtggaat.....ataactgtgtaattctaga 741

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_23Sep04:\*

- 1: Geneseq1980s:\*
- 2: Geneseq1990s:\*
- 3: Geneseq2000s:\*
- 4: Geneseq2001as:\*
- 5: Geneseq2001bs:\*
- 6: Geneseq2002as:\*
- 7: Geneseq2002bs:\*
- 8: Geneseq2003as:\*
- 9: Geneseq2003bs:\*
- 10: Geneseq2003cs:\*
- 11: Geneseq2003ds:\*
- 12: Geneseq2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	739	99.7	741	3	AA15569 Phaffia r
2	152	20.5	1904	2	AAV60108 Rhizocton
3	150.4	20.3	1793	2	AAV60107 Rhizocton
4	145.4	19.6	1247	10	ACA61067 Phyllost
5	142	19.2	9558	2	AAQ8228 Valencia
6	140	18.9	913	11	ADM45469 Insect re
7	138.2	18.7	1821	2	AAV54087 Nucleotid
8	136	18.4	1734	5	ABK49559 Putrefact
9	134.6	18.2	5373	2	AAV31379 Arabidops
10	134.6	18.2	59590	3	AAF22281 BAC conta
11	132.2	17.8	3172	10	ADF54865 Ribosomal
12	131.6	17.8	703	2	ADR01486 A. gossyp
13	131.6	17.8	706	2	ADR02122 A. gossyp
14	131.6	17.8	717	2	ADR01910 A. gossyp
15	130	17.5	712	2	ADR02218 A. gossyp
16	130	17.5	2089	8	ABZ20764 Muscodor
17	128.4	17.3	1761	6	ABV78699 C. crassi
18	128.4	17.3	1766	6	ABV78720 C. sinens
19	128.4	17.3	1766	6	ABV78708 C. sinens
20	128.4	17.3	1766	6	ABV78714 C. sinens
21	128.4	17.3	1766	6	ABV78711 C. sinens

22	128.4	17.3	1766	6	ABV78717 C. sinens
23	128.4	17.3	1766	6	ABV78705 C. sinens
24	128.4	17.3	1766	6	ABV78702 C. sinens
25	128.4	17.3	1766	6	ABV78723 C. sinens
26	128.4	17.3	1771	2	AAV61668 Fusarium
27	126.8	17.1	568	3	AAF11545 Aspergill
28	126.2	17.0	1840	2	AAV54086 Nucleotid
c 29	125.6	17.0	3420	6	ABA99033 Saccharom
30	119.2	16.1	367	8	ABX43439 Bovine ES
c 31	119	16.1	570	3	AAF08498 Fusarium
32	118.6	16.0	2055	8	ABZ20766 Muscodor
33	117.8	15.9	873	11	ADM44838 Insect re
34	117	15.8	717	11	ADM45463 Insect re
35	117	15.8	1737	8	AA151417 Spongipel
36	116.8	15.8	1776	4	AAF25849 S. exigui
37	115.4	15.6	617	3	AAF10913 Fusarium
38	114.6	15.5	1750	2	AAAT90818 C. parvum
39	114.6	15.5	1750	3	AA46368 Nucleotid
40	114.6	15.5	1798	4	AAAD14297 Yeast DNA
41	114.6	15.5	1798	5	AAAD14004 DNA to in
42	113.6	15.3	1802	5	AAF23018 Yeast 18S
c 43	113.6	15.3	723	2	ADR02260 A. gossyp
44	112.6	15.2	762	10	ADK54329 Plant DNA
45	112.6	15.2	1878	10	ADK57663 Plant DNA

## ALIGNMENTS

## RESULT 1

AA15569  
ID AAA15569 standard; DNA; 741 BP.  
XX  
AC AAA15569;  
XX  
DT 15-SEP-2003 (revised)  
25-SEP-2000 (first entry)  
XX  
DE Phaffia rhodozyma rDNA gene.  
XX  
KW Yeast; ribosomal DNA; rDNA; non-transcription spacer; NTS;  
selectable marker; ribosomal DNA; db.  
XX  
OS Xanthophyllomyces dendrorhous.  
XX  
PN WO200026387-A1.  
XX  
PD 11-MAY-2000.  
XX  
PF 29-MAY-1999; 99WO-KR000265.  
XX  
PR 31-OCT-1998; 98KR-00046547.  
XX  
PA (ROAD ) KOREA ADV INST SCI & TECHNOLOGY.  
(HAIT-) HAI TAI CONFECTIONERY CO LTD.  
XX  
PI Choi E, Rhee S, Sohn J, Park S, Lee YH, Lee SJ, Jang JK;  
Choi SK, Son YR;  
XX  
DR WPI; 2000-365630/31.  
XX  
PT Novel vector comprising a cyclohexamide-resistance gene and a ribosomal  
DNA useful for the transformation of Phaffia rhodozyma.  
XX  
PS Claim 5; Page 38-39; 43pp; English.  
XX  
CC The present sequence is a Phaffia rhodozyma rDNA gene. This sequence can  
be used to enhance the integration efficiency of foreign DNA into host  
genomes. This is because the rDNA is highly repeated as tandem units in  
eukaryotic genomes. This rDNA also has a non-transcription spacer (NTS),  
i.e. a DNA spacer between transcribed DNA. This NTS may be used as a  
component of a transforming vector, which also has a selectable marker  
and a foreign gene. The wild-type Phaffia rhodozyma L41 gene, which



XX 28-FEB-1997; 97JP-00062106.  
 XX (SHIN-) SHINKINRUI KINO KAIHATSU KENKYUSHO KK.  
 XX WPI; 1998-535035/46.  
 XX Use of oligo:nucleotide for detecting or identifying fungus of  
 FT Rhizoctonia genus - used to detect or identify fungus rapidly and  
 PT exactly.  
 XX Example 1; Page 8; 24pp; Japanese.  
 XX The present sequence appears in the specification, which describes  
 CC oligonucleotide probes for detecting or identifying of a fungus of  
 CC Rhizoctonia genus. The sequences are derived from the 18S rRNA gene  
 CC sequence, and are unique to Rhizoctonia species. (Updated on 17-OCT-2003  
 CC to standardise OS field)  
 XX SQ Sequence 1793 BP; 460 A; 363 C; 463 G; 490 T; 0 U; 17 Other;  
 Query Match 20.3%; Score 150.4; DB 2; Length 1793;  
 Best Local Similarity 96.2%; Pred. No. 1.5e-38;  
 Matches 154; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
 Qy 582 CTGTTGATCTGCCAGTAGTCATATGCTTCTCTCAAGATTAAGCCATGCTCTAAG 641  
 Db 1 CTGTTGATCTGCCAGTAGTCATATGCTTCTCTCAAGATTAAGCCATGCTCTAAG 60  
 Qy 642 TATAACAAATTCATCTGGAACCTGGAATGCTCAATTAATCAGTTATTTT 701  
 Db 61 TATAACAACTTTTGTACTGTGGAACCTGGAATGCTCAATTAATCAGTTATTTT 120  
 Qy 702 GATGTAATCTTGTACATGATTAATCTGTTGTAATCTTCTAGA 741  
 Db 121 GATGTAATCTTGTACATGATTAATCTGTTGTAATCTTCTAGA 160  
 RESULT 4  
 ID ACA61067 standard; DNA; 1247 BP.  
 AC ACA61067;  
 XX DT. 14-JUL-2003 (first entry)  
 XX Phyllosticta ribosomal DNA intergenic sequence (IGS).  
 DE Guignardia; pathogen; internal transcribed spacer; ITS; citrus fruit;  
 KW intergenic sequence; intronic sequence; calmodulin; chitin synthase;  
 KW citrus blackspot; phyllosticta; intergenic sequence; IGS; ds.  
 XX Phyllosticta sp.  
 XX WO2003031933-A2.  
 XX 17-APR-2003.  
 XX 09-OCT-2002; 2002WO-US032227.  
 XX 09-OCT-2001; 2001US-0327982P.  
 XX (UYOR-) UNIV OREGON.  
 XX Carroll GC;  
 XX WPI; 2003-372133/35.  
 XX Differentiating pathogenic and non-pathogenic *Guignardia* sp., by  
 FT assessing hybridization between DNA from *Guignardia*-infected citrus and  
 FT probes based on intronic sequences from calmodulin and chitin synthase  
 XX genes.

PS Example 2; Fig 3; 37pp; English.  
 XX The invention describes a method of differentiating pathogenic and non-  
 CC pathogenic species of *Guignardia* (I). The method comprises obtaining a  
 CC DNA sample from a citrus fruit infected with (I), immobilising the DNA,  
 CC probing the immobilised DNA with a probe based on intergenic sequences  
 CC and intronic sequences from within the calmodulin and chitin synthase  
 CC genes, and demonstrating hybridisation with the probes to represent the  
 CC pathogenic species and non-pathogenic species. The method is specific,  
 CC rapid and useful for differentiating pathogenic species (e.g. *Guignardia*  
 CC *citricarpa*, the causative agent of citrus blackspot) from non-pathogenic  
 CC species of *Guignardia*. This sequence represents a phyllosticta ribosomal  
 CC DNA intergenic sequence used to examine if ribosomal DNA intergenic  
 CC sequences are species-specific and can therefore be used to differentiate  
 CC between pathogenic and non-pathogenic species of *Guignardia*  
 XX SQ Sequence 1247 BP; 253 A; 336 C; 352 G; 306 T; 0 U; 0 Other;  
 Query Match 19.6%; Score 145.4; DB 10; Length 1247;  
 Best Local Similarity 90.7%; Pred. No. 5.8e-37;  
 Matches 166; Conservative 0; Mismatches 16; Indels 1; Gaps 1;  
 Qy 559 CCCTCTCTCTCTGCGATAGTTACCTGTTGATCTGCGAGTAGTCATATGCTTGTCTCAA 618  
 Db 450 CCCTGCGGCTCAAGATAGTTACCTGTTGATCTGCGAGTAGTCATATGCTTGTCTCAA 509  
 Qy 619 AGATTAAAGCCATGATCTCTAAAGTATTAACAAATTCATCTGTGAACTGCGAATGGCTC 678  
 Db 510 AGATTAAAGCCATGATCTCTAAAGTATTAAGC-AACTATATCTGTGAACTGCGAATGGCTC 568  
 Qy 679 ATTAAATCAGTTATAGTTTATTTGATGCTTGTGCTTGTGCTGATGATTAATCTGTTCT 738  
 Db 569 ATTAAATCAGTTATAGTTTATTTTTCATAGTACCTTACTTCTGATACCGTGGTAATCT 628  
 Qy 739 AGA 741  
 Db 629 AGA 631  
 RESULT 5  
 ID AAQ88228 standard; DNA; 9558 BP.  
 XX AAQ88228;  
 XX AC  
 XX DT. 27-AUG-2003 (revised)  
 XX 24-NOV-1995 (first entry)  
 XX Valencia orange ribosomal RNA gene.  
 DE Ribosomal RNA; rRNA; 18S; 28S; 5.8S; Valencia orange; RFLP analysis;  
 KW DNA fingerprinting; restriction fragment length polymorphism; ds.  
 XX Citrus.  
 XX Key Location/Qualifiers  
 FH 1. .1597  
 FT misc\_RNA /tag= a  
 FT /product= "18S\_rRNA"  
 FT 1598. .1848  
 FT misc\_RNA /tag= b  
 FT /function= "spacer"  
 FT 1849. .2011  
 FT misc\_RNA /tag= c  
 FT /product= "5.8S\_rRNA"  
 FT 2012. .2238  
 FT /tag= d  
 FT /function= "spacer"  
 FT 2239. .5582  
 FT misc\_RNA /tag= e  
 FT /product= "28S\_rRNA"  
 FT 5583. .9396  
 FT misc\_RNA /tag= f



XX JPI0234399-A.  
 XX 08-SEP-1998.  
 XX 28-FEB-1997; 97JP-00062114.  
 XX 28-FEB-1997; 97JP-00062114.  
 XX (SHIN-) SHINKINRUI KINO KAIHATSU KENKYUSHO KK.  
 XX WPI; 1998-535049/46.  
 XX New oligo-nucleotide probe - for rapid and precise detection and  
 XX identification of Pythium genus fungus.  
 XX Disclosure; Page 9; 22pp; Japanese.  
 XX This is the nucleotide sequence of the Pythium spinosum OPA-1 used in the  
 XX method of the invention where novel probes are used for the detection and  
 XX identification of a fungus of Pythium genus  
 XX Sequence 1821 BP; 460 A; 329 C; 466 G; 518 T; 0 U; 48 Other;  
 XX  
 XX Query Match 18.7%; Score 138.2; DB 2; Length 1821;  
 XX Best Local Similarity 91.2%; Pred. No. 1.7e-34;  
 XX Matches 146; Conservative 0; Mismatches 14; Indels 0; Gaps 0;  
 XX  
 XX 582 CTGCTTGATCTGCCAGTAGTCATATGCTGTCTCAAGATTAAAGCCATGCATGCTAAG 641  
 XX 1 CTGCTTGATCTGCCAGTAGTCATATGCTGTCTCAAGATTAAAGCCATGCATGCTAAG 60  
 XX  
 XX 642 TATAAACAATTTCTACTGTGAACTGCGAATGCTCAATTAAGTAAATCAGTTATAGTTATTT 701  
 XX 61 TATAAACAATTTCTACTGTGAACTGCGAATGCTCAATTAAGTAAATCAGTTATAGTTATTT 120  
 XX  
 XX 702 GATGCTACTTGTACATGATGATGCTCAATTAAGTAAATCAGTTATAGTTATTT 741  
 XX 121 GATAGTACCTTACTACTTGGTAAACCGTAGTAATTTCTAGA 160  
 XX  
 XX RESULT 8  
 XX ABK49559  
 XX ID ABK49559 standard; DNA; 1734 BP.  
 XX AC  
 XX ABK49559;  
 XX 15-JUL-2002 (first entry)  
 XX  
 XX Putrefactive microbe associated polynucleotide.  
 XX  
 XX Putrefactive microbe; halotolerant; manganese peroxidase;  
 XX paper-pulp industry; dyeing industry; industrial waste treatment; ds.  
 XX  
 XX Phlebia sp.  
 XX  
 XX JP2001169775-A.  
 XX 26-JUN-2001.  
 XX  
 XX 06-OCT-2000; 2000JP-00307045.  
 XX  
 XX 06-OCT-1999; 99JP-00285955.  
 XX (MEIJ ) MEIJI SEIKA KAISHA LTD.  
 XX  
 XX WPI; 2001-608873/70.  
 XX  
 XX New microbe for decomposing substances and bleaching pulps, comprises a  
 XX microbe that produces halotolerant manganese peroxidase.  
 XX Claim 4; Page 9; 11pp; Japanese.  
 XX

CC The invention describes a white putrefactive microbe having halotolerant  
 CC manganese peroxidase activity. The microbe strain can be used in the  
 CC paper-pulp industry, dyeing industry, and process of treating industrial  
 CC waste. This sequence represents a putrefactive microbe associated  
 CC polynucleotide. Note: This sequence does not encode the peptide shown in  
 CC AAU79900  
 XX  
 XX Sequence 1734 BP; 444 A; 348 C; 467 G; 475 T; 0 U; 0 Other;  
 XX  
 XX Query Match 18.4%; Score 136; DB 5; Length 1734;  
 XX Best Local Similarity 96.5%; Pred. No. 9e-34;  
 XX Matches 139; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 XX  
 XX 598 GTAGTCATATGCTTGTCTCAAGATTAAAGCCATGCATGCTAAGTATAAACAAGTTCTGA 657  
 XX 1 GTAGTCATATGCTTGTCTCAAGATTAAAGCCATGCATGCTAAGTATAAACAAGTTCTGA 60  
 XX  
 XX 658 CTGTGAACTCGCAATGCTCAATTAAGTAAATCAGTTATAGTTATTTGATGCTACCTTGCTAC 717  
 XX 61 CTGTGAACTCGCAATGCTCAATTAAGTAAATCAGTTATAGTTATTTGATGCTACCTTGCTAC 120  
 XX  
 XX 718 ATGCATAACTGTGCTAAATTTCTAGA 741  
 XX 121 ATGCATAACTGTGCTAAATTTCTAGA 144  
 XX  
 XX RESULT 9  
 XX AAV31379  
 XX ID AAV31379 standard; DNA; 5373 BP.  
 XX AC  
 XX AAV31379;  
 XX 07-SEP-1998 (first entry)  
 XX  
 XX Arabidopsis thaliana rRNA gene intergenic region.  
 XX  
 XX Arabidopsis thaliana; rRNA gene; ribosomal DNA; intergenic region;  
 XX DNA-construct; plant; multiple Sali repeat; stability; copy number;  
 XX transgene; antibody; insecticidal protein; Bt toxin; ds.  
 XX  
 XX Arabidopsis thaliana.  
 XX  
 XX Key Location/Qualifiers  
 XX misc\_feature 1..485  
 XX /tag= a  
 XX /note= "25S rDNA 3'-end"  
 XX 486..5211  
 XX /tag= b  
 XX /note= "intergenic region"  
 XX 1263..1557  
 XX /tag= c  
 XX /note= "Sali box 1"  
 XX 1883..2177  
 XX /tag= d  
 XX /note= "Sali box 2"  
 XX 2503..3003  
 XX /tag= e  
 XX /note= "Sali box 3"  
 XX 5212..5373  
 XX /tag= f  
 XX /note= "18S rDNA 5'-end"  
 XX  
 XX WO9813505-A1.  
 XX 02-APR-1998.  
 XX 23-SEP-1997; 97WO-EP005217.  
 XX 24-SEP-1996; 96AT-00001695.  
 XX (PLBZ ) PLANT GENETIC SYSTEMS NV.  
 XX Bachmair A, Schweizer D;  
 XX





CC spacer region containing DNA is useful as an enhancer which activates the  
 CC promoter of foreign cell. The invention also provides a method for  
 CC increasing expression in one or more foreign cell(s) in one or more  
 CC organ(s) of plant, by increasing activity of the promoter of one or more  
 CC foreign gene involving the use of the spacer region containing DNA; a  
 CC chimeric gene containing the spacer region containing DNA and a gene  
 CC promoter, coding sequence or non-coding sequence and a terminator sequence;  
 CC a transformed plant containing the chimeric gene; and a cell in which  
 CC expression of a foreign gene is increased by the novel methods of the  
 CC invention. This polynucleotide represents a rice DNA sequence used in the  
 CC novel spacer region DNA utilising method of the invention.

CC SQ Sequence 3172 BP; 591 A; 1047 C; 1041 G; 493 T; 0 U; 0 Other;

Query Match 17.8%; Score 132.2; DB 10; Length 3172;

Best Local Similarity 91.5%; Pred. No. 2.3e-32;

Matches 151; Conservative 0; Mismatches 13; Indels 1; Gaps 1;

Qy 577 GTTACCTGGTTGATCCTGCCAGTAGTCATATGCTGTCTCAAGATTAAAGCCATGCTGT 636

Db 2623 GCTACCTGGTTGATCCTGCCAGTAGTCATATGCTGTCTCAAGATTAAAGCCATGCTGT 2682

Qy 637 CTAAGTATAAACAAATTCATATCTGTGAACCTGCGAATGGCTCATTTAAATCAGTTTATAGTT 696

Db 2683 GCAAGTAGAAGTAATTCGAACCTGTGAACCTGCGAATGGCTCATTTAAATCAGTTTATAGTT 2742

Qy 697 TATTTGATGGTACCTTGCTACATGGAATAACTGTGGTAAATCTTCTAGA 741

Db 2743 TGTTTGATGGTA-CGTGCTACTCGGATAACCGTAGTAATCTTCTAGA 2786

#### RESULT 12

ADRO1486/c

ID ADRO1486 standard; DNA; 703 BP.

XX AC ADRO1486;

DT 23-SEP-2004 (first entry)

DE A. gossypii genomic DNA PAG1070RP.

XX Filamentous funghi; ds; forensic identification; gene characterisation;  
 XX intergenomic comparison; chromosome mapping.

XX Erethothecium gossypii.

XX US6239264-B1.

XX 29-MAY-2001.

XX 24-DEC-1997; 97US-00998416.

XX 31-DEC-1996; 97CH-00000016.

XX (SYNG-) SYNGENTA PARTICIPATIONS AG.

XX Philippsen P, Poehlmann R, Steiner-Lange S, Mohr C, Wendland J;

XX Knechtle P, Reibischung C;

XX WPI; 1998-388120/33.

XX New gene for adenylate cyclase from *Ashbya gossypii* - useful for  
 PT generating recombinant microorganisms with alteration in gene of camp-  
 PT dependent signalling pathway for increasing production of fine chemicals.

XX Example 3; SEQ ID NO 178; 632pp; English.

XX The invention relates to isolated DNA molecules comprising isolated  
 CC genomic DNA sequences from the filamentous funghi *Ashbya gossypii*, the  
 CC sequences comprising ADRO1309, ADRO1366, ADRO1367, ADRO1388, ADRO1428,  
 CC ADRO1466, ADRO1629, ADRO1637, ADRO2057, ADRO2345 and ADRO2369, chosen  
 CC from 1047 disclosed genomic sequences. Also included is a cloning vector  
 CC comprising a nucleotide sequence chosen from the above sequences. The  
 CC invention relates to isolated DNA molecules comprising isolated

CC novel *Ashbya gossypii* genomic sequences are useful for forensic  
 CC identification, gene characterisation, for studying gene organisation by  
 CC intergenomic comparison (with *Saccharomyces cerevisiae*), identifying  
 CC biosynthetic genes for selectable markers, to isolate  
 CC promoters/terminators/centromeres, chromosome mapping, and in identifying  
 CC sequences unique to *Ashbya gossypii* for species identification. The  
 CC present sequence is an *A. gossypii* novel genomic sequence of the  
 CC invention.

CC SQ Sequence 703 BP; 210 A; 165 C; 129 G; 197 T; 0 U; 2 Other;

Query Match 17.8%; Score 131.6; DB 2; Length 703;

Best Local Similarity 93.5%; Pred. No. 1.6e-32;

Matches 159; Conservative 0; Mismatches 9; Indels 2; Gaps 2;

Qy 573 GATAGTTACCTGGTTGATCCTGCCAGTAGTCATATGCTGTCTCAAGATTAAAGCCATGTC 632

Db 686 GATAGTTATCTGGTTGATCCTGCCAGTAGTCATATGCTGTCTCAAGATTAAAGCCATGTC 627

Qy 633 ATGCTAAGTATAAACAAATTCATATCTGTGAAACTGCGAATGGCTCATTTAAATCAGTTAT 692

Db 626 ATGCTAAGTATAGC-AAITTTATACAGTGAACCTGCGAATGGCTCATTTAAATCAGTTAT 568

Qy 693 AGTTTATTCATGTACC-TTGCTACATGGATACCTGTGTAATCTTCTAGA 741

Db 567 CGTTTATTCATAGTTCCTTTACTACATGGATATCTGTGTAATCTTCTAGA 518

#### RESULT 13

ADRO2122

ID ADRO2122 standard; DNA; 706 BP.

XX AC ADRO2122;

DT 23-SEP-2004 (first entry)

DE A. gossypii genomic DNA PAG1518UP.

XX Filamentous funghi; ds; forensic identification; gene characterisation;  
 XX intergenomic comparison; chromosome mapping.

XX Erethothecium gossypii.

XX US6239264-B1.

XX 29-MAY-2001.

XX 24-DEC-1997; 97US-00998416.

XX 31-DEC-1996; 97CH-00000016.

XX (SYNG-) SYNGENTA PARTICIPATIONS AG.

XX Philippsen P, Poehlmann R, Steiner-Lange S, Mohr C, Wendland J;

XX Knechtle P, Reibischung C;

XX WPI; 1998-388120/33.

XX New gene for adenylate cyclase from *Ashbya gossypii* - useful for  
 PT generating recombinant microorganisms with alteration in gene of camp-  
 PT dependent signalling pathway for increasing production of fine chemicals.

XX Example 3; SEQ ID NO 814; 632pp; English.

XX The invention relates to isolated DNA molecules comprising isolated  
 CC genomic DNA sequences from the filamentous funghi *Ashbya gossypii*, the  
 CC sequences comprising ADRO1309, ADRO1367, ADRO1388, ADRO1428,  
 CC ADRO1466, ADRO1629, ADRO1637, ADRO2057, ADRO2345 and ADRO2369, chosen  
 CC from 1047 disclosed genomic sequences. Also included is a cloning vector  
 CC comprising a nucleotide sequence chosen from the above sequences. The  
 CC novel *Ashbya gossypii* genomic sequences are useful for forensic  
 CC identification, gene characterisation, for studying gene organisation by  
 CC intergenomic comparison (with *Saccharomyces cerevisiae*), identifying

CC biosynthetic genes for selectable markers, to isolate  
CC promoters/terminators/centromeres, chromosome mapping, and in identifying  
CC sequences unique to *Ashbya gossypii* for species identification. The  
CC present sequence is an *A. gossypii* novel genomic sequence of the  
CC invention.

XX SQ Sequence 706 BP; 180 A; 146 C; 171 G; 209 T; 0 U; 0 Other;  
Query Match 17.8%; Score 131.6; DB 2; Length 706;  
Best Local Similarity 93.5%; Pred. No. 1.6e-32;  
Matches 159; Conservative 0; Mismatches 9; Indels 2; Gaps 2;  
QY 573 GATAGTTACCTGGTTGATCTGCCAGTAGTCATATGCTTCTCAAGATTAAAGCCATGC 632  
DB 499 GATAGTTATCTGGTTGATCTGCCAGTAGTCATATGCTTCTCAAGATTAAAGCCATGC 558  
QY 633 ATGCTTAAGTATAACAAATTCATCTGTGGAACCTGCGAATGGCTCATTTAAATCAGTTAT 692  
DB 559 ATGCTTAAGTATAAGC-AAATTTATACAGTGAACCTGCGAATGGCTCATTTAAATCAGTTAT 617  
QY 693 AGTTTATTGATGTACC-TTGCTACATGGATTAACCTGGTAAATTCCTAGA 741  
DB 618 CGTTTATTGATAGTTCTTACTACATGGATATCTGTGGTAAATTCCTAGA 667

## RESULT 14

ADRL01910  
ID ADR01910 standard; DNA; 717 BP.  
XX AC  
XX ADR01910;  
XX DT 23-SEP-2004 (first entry)  
XX DE A. gossypii genomic DNA PAG1411UP.  
XX KW Filamentous funghi; ds; forensic identification; gene characterisation;  
XX intergenomic comparison; chromosome mapping.  
XX OS Eremothecium gossypii.  
XX FN US6239264-B1.  
XX PD 29-MAY-2001.  
XX PF 24-DEC-1997; 97US-00998416.  
XX PR 31-DEC-1996; 97CH-00000016.  
XX PA (SYNG-) SYNGENTA PARTICIPATIONS AG.  
XX PI Philippsen P, Poehlmann R, Steiner-Lange S, Mohr C, Wendland J;  
PI Knechtle P, Rebischung C;  
XX WPI; 1998-388120/33.  
XX PT New gene for adenylate cyclase from *Ashbya gossypii* - useful for  
XX generating recombinant microorganisms with alteration in gene of cAMP-  
XX dependent signalling pathway for increasing production of fine chemicals.  
XX PS Example 3; SEQ ID NO 602; 632pp; English.  
XX CC The invention relates to isolated DNA molecules comprising isolated  
XX genomic DNA sequences from the filamentous funghi *Ashbya gossypii*, the  
XX sequences comprising ADR01309, ADR01366, ADR01367, ADR01388, ADR01428,  
XX ADR01466, ADR01629, ADR01637, ADR02057, ADR02345 and ADR02369, chosen  
XX from 1047 disclosed genomic sequences. Also included is a cloning vector  
XX comprising a nucleotide sequence chosen from the above sequences. The  
XX novel *Ashbya gossypii* genomic sequences are useful for forensic  
XX identification, gene characterisation, for studying gene organisation by  
XX intergenomic comparison (with *Saccharomyces cerevisiae*), identifying  
XX biosynthetic genes for selectable markers, to isolate  
XX promoters/terminators/centromeres, chromosome mapping, and in identifying  
XX sequences unique to *Ashbya gossypii* for species identification. The

CC present sequence is an *A. gossypii* novel genomic sequence of the  
CC invention.

XX SQ Sequence 717 BP; 186 A; 145 C; 172 G; 214 T; 0 U; 0 Other;  
Query Match 17.8%; Score 131.6; DB 2; Length 717;  
Best Local Similarity 93.5%; Pred. No. 1.6e-32;  
Matches 159; Conservative 0; Mismatches 9; Indels 2; Gaps 2;  
QY 573 GATAGTTACCTGGTTGATCTGCCAGTAGTCATATGCTTCTCAAGATTAAAGCCATGC 632  
DB 498 GATAGTTATCTGGTTGATCTGCCAGTAGTCATATGCTTCTCAAGATTAAAGCCATGC 557  
QY 633 ATGCTTAAGTATAACAAATTCATCTGTGGAACCTGCGAATGGCTCATTTAAATCAGTTAT 692  
DB 558 ATGCTTAAGTATAAGC-AAATTTATACAGTGAACCTGCGAATGGCTCATTTAAATCAGTTAT 616  
QY 693 AGTTTATTGATGTACC-TTGCTACATGGATTAACCTGGTAAATTCCTAGA 741  
DB 617 CGTTTATTGATAGTTCTTACTACATGGATATCTGTGGTAAATTCCTAGA 666

## RESULT 15

ADRL02218  
ID ADR02218 standard; DNA; 712 BP.  
XX AC  
XX ADR02218;  
XX DT 23-SEP-2004 (first entry)  
XX DE A. gossypii genomic DNA PAG1567UP.  
XX KW Filamentous funghi; ds; forensic identification; gene characterisation;  
XX intergenomic comparison; chromosome mapping.  
XX OS Eremothecium gossypii.  
XX FN US6239264-B1.  
XX PD 29-MAY-2001.  
XX PF 24-DEC-1997; 97US-00998416.  
XX PR 31-DEC-1996; 97CH-00000016.  
XX PA (SYNG-) SYNGENTA PARTICIPATIONS AG.  
XX PI Philippsen P, Poehlmann R, Steiner-Lange S, Mohr C, Wendland J;  
PI Knechtle P, Rebischung C;  
XX WPI; 1998-388120/33.  
XX PT New gene for adenylate cyclase from *Ashbya gossypii* - useful for  
XX generating recombinant microorganisms with alteration in gene of cAMP-  
XX dependent signalling pathway for increasing production of fine chemicals.  
XX PS Example 3; SEQ ID NO 910; 632pp; English.  
XX CC The invention relates to isolated DNA molecules comprising isolated  
XX genomic DNA sequences from the filamentous funghi *Ashbya gossypii*, the  
XX sequences comprising ADR01309, ADR01366, ADR01367, ADR01388, ADR01428,  
XX ADR01466, ADR01629, ADR01637, ADR02057, ADR02345 and ADR02369, chosen  
XX from 1047 disclosed genomic sequences. Also included is a cloning vector  
XX comprising a nucleotide sequence chosen from the above sequences. The  
XX novel *Ashbya gossypii* genomic sequences are useful for forensic  
XX identification, gene characterisation, for studying gene organisation by  
XX intergenomic comparison (with *Saccharomyces cerevisiae*), identifying  
XX biosynthetic genes for selectable markers, to isolate  
XX promoters/terminators/centromeres, chromosome mapping, and in identifying  
XX sequences unique to *Ashbya gossypii* for species identification. The  
XX present sequence is an *A. gossypii* novel genomic sequence of the  
XX invention.

SQ Sequence 712 BP; 184 A; 145 C; 170 G; 213 T; 0 U; 0 Other;

Query Match 17.5%; Score 130; DB 2; Length 712;  
Best Local Similarity 92.9%; Pred. No. 5.4e-32;  
Matches 158; Conservative 0; Mismatches 10; Indels 2; Gaps 2;

Qy 573 GATAGTTACCTGGTTGATCCTGCCAGTAGTCATATGTTGTTCTCAAGATTAAAGCCATGC 632  
Db 498 GATAGTTATCTGGTTGATCCTGCCAGTAATCATATGCTTGTCTCAAGATTAAAGCCATGC 557

Qy 633 ATGCTAAGTATAAACAATAATTCATACTGTGAAACTGGGAATGGCTCATTTAAATCAGTTAT 692  
Db 558 ATGCTAAGTATAAGC-AAATTATACAGTGAACCTGGGAATGGCTCATTTAAATCAGTTAT 616

Qy 693 AGTTTATTGATGGTACC-TTGCTACATGGATAACTGTGGTAAATCTAGA 741  
Db 617 CGTTTATTGATAGTTCTCTTACTACATGGATATCTGTGGTAAATCTAGA 666

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Job time : 453.315 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: January 18, 2005, 08:42:24 ; Search time 5798.42 Seconds  
(without alignments)  
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Title: US-09-830-691A-1  
Perfect score: 1223  
Sequence: 1 atgtgcacgttcccaagac.....gagcgcgcattctttcttaa 1223

Scoring table: IDENTITY NUC  
Gapop 10'0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.\*  
1: gb\_ba.\*  
2: gb\_htg.\*  
3: gb\_in.\*  
4: gb\_on.\*  
5: gb\_ov.\*  
6: gb\_pat.\*  
7: gb\_ph.\*  
8: gb\_pl.\*  
9: gb\_pr.\*  
10: gb\_ro.\*  
11: gb\_sta.\*  
12: gb\_sy.\*  
13: gb\_un.\*  
14: gb\_vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1223	100.0	1223	6	BD237786 Phaffiarh
2	1215	99.3	2552	8	AF004672 Xanthophy
3	147.6	12.1	350	6	BD237787 Phaffiarh
4	115	9.4	336	8	CRU31912 Chlamydomon
5	113.8	9.3	110000	8	CR382128_05 Continuation (6 of
6	107.8	8.8	688	6	AK382552 Sequence
7	107.8	8.8	1048	8	D10153 Pichia guil
8	107.8	8.8	1048	6	YSRQLAF M62395 Pichia sp.
9	107.8	8.8	2086	6	AR065319 Sequence
10	107.8	8.8	2086	6	E11620 Candida uti
11	107.8	8.8	2086	6	AR382551 Sequence
12	107.8	8.8	2086	8	YSAREPL41 D67040 Candida uti
13	103.4	8.5	444	8	RIC340 D10406 Rice mRNA f
14	103.4	8.5	676	8	AK058924 Oryza sat
15	103.4	8.5	2173	8	AK069083 Oryza sat
16	102.8	8.4	1611	8	AB021315 Coprinus
17	101.4	8.3	110000	8	CH380953_05 Continuation (6 of
18	101	8.3	388	5	AY099511 Danio rer
19	101	8.3	480	8	CNS018R9 AL110700 Botrytis

20	101	8.3	480	8	CNS01A80	AL112624 Botrytis
21	101	8.3	480	8	CNS01AXH	AL113517 Botrytis
22	101	8.3	516	8	CNS01AGD	AL112901 Botrytis
23	101	8.3	518	8	CNS0190P	AL111040 Botrytis
24	101	8.3	540	8	CNS019IQ	AL111690 Botrytis
25	101	8.3	540	8	CNS01AOU	AL112342 Botrytis
26	101	8.3	540	8	CNS01C7X	AL115189 Botrytis
27	101	8.3	540	8	CNS01CSO	AL115936 Botrytis
28	101	8.3	540	8	CNS01D75	AL116457 Botrytis
29	101	8.3	540	8	CNS01DEP	AL116729 Botrytis
30	101	8.3	540	8	CNS01DN9	AL117037 Botrytis
31	101	8.3	636	8	CNS01D5A	AL116390 Botrytis
32	101	8.3	681	5	EC055187	BC055187 Danio rer
33	101	8.3	840	8	CNS01BEI	AL114130 Botrytis
34	100.6	8.2	1828	8	YSKKFL41	D10580 Kluyveromyc
35	99.8	8.2	321	5	AJ605265	AJ605265 Platichth
36	99	8.1	12855	8	SPAC15E1	AL109770 S.pombe c
37	98.2	8.0	412	5	AF401592	AF401592 Ictalurus
38	98.2	8.0	1333	6	AX073124	AX073124 Sequence
39	98.2	8.0	1975	8	YSCSCL41A	D10578 Saccharomyc
40	98.2	8.0	2523	8	SCYNL162W	271438 S.cerevisia
41	98.2	8.0	36813	8	SCORFSC14	X92517 S.cerevisia
42	97.8	8.0	306906	8	AE016900	AE016900 Ermothec
43	96.6	7.9	1262	6	AX073018	AX073018 Sequence
44	96.6	7.9	1823	8	YSCSCL41B	D10579 Saccharomyc
45	96.6	7.9	30350	8	YSCH9315	U10398 Saccharomyc

ALIGNMENTS

RESULT 1  
LOCUS BD237786 1223 bp DNA linear PAT 17-JUL-2003  
DEFINITION Phaffiarhodozyma transforming vectors and transforming method  
thereof.  
ACCESSION BD237786  
VERSION BD237786.1 GI:33047556  
KEYWORDS JP 2002528124-A/1.  
SOURCE Xanthophyllomyces dendrorhous (anamorph: Phaffia rhodozyma)  
ORGANISM Xanthophyllomyces dendrorhous  
Eukaryota; Fungi; Basidiomycota; Hymenomycetes;  
Heterobasidiomycetes; Tremellomycetidae; Cystofilobasidiales;  
Cystofilobasidiaceae; Xanthophyllomyces.  
REFERENCE 1 (bases 1 to 1223)  
AUTHORS Choi,E.S., Rhee,S.K., Sohn,J.H., Park,S.D., Lee,Y.H., Lee,S.J.,  
Jang,J.K., Choi,S.K. and Son,Y.R.  
TITLE Phaffiarhodozyma transforming vectors and transforming method  
JOURNAL Patent: JP 2002528124-A 1 03-SEP-2002;  
KOREA INSTITUTE OF SCIENCE AND TECHNOLOGY, HAITAI CONFECTIONERY CO  
LTD  
COMMENT OS Phaffia rhodozyma  
PN JP 2002528124-A/1  
PD 03-SEP-2002  
PR 29-MAY-1999 JP 2000579759  
PF 31-OCT-1998 KR 1998/46547  
PI EUI SUNG CHOI,SANG KI RHEE,JUNG HOON SOHN,SOO DONG PARK,YOON  
PI HYOUNG LEE  
PI SEUNG JAE LEE, JAE KWEON JANG, SEOK KEUN CHOI, YOUNG ROK SON PC  
C12N15/09,C12N1/19//C12N1/19,C12R1:645),C12N15/00 CC  
Phaffiarhodozyma transforming vectors and transforming method CC  
thereof  
FH Key Location/Qualifiers  
FT source 1..1223  
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/db\_xref='taxon:5421'  
ORIGIN  
Query Match 100.0%; Score 1223; DB 6; Length 1223;

ORIGIN

Query Match	99.3%;	Score 1215;	DB 8;	Length 2552;
Best Local Similarity	99.6%;	Pred. NO. 0;		
Matches 1218;	Conservative	0;	Mismatches 5;	Indels 0;
Gaps	0;			

On 1 ATGGTCAACGTTCCCAAGACTCGACGTCGAGTTATAGCAAAATTCAAACAACCTCCACAGCA 60



Db 845 ATGGTCAACAGTTCACCAAGACTCGAGTGTATAGCAATTTCAACAACTCTCAGACGA 904  
Qy 61 CAATATATCCAGTGCATCGAAGAGTTTGTGGATAAAGCGACAGTGTTCAGAGGGAAGAG 120  
Db 905 CAATATATCCAGTGCATCGAAGAGTTTGTGGATAAAGCGACAGTGTTCAGAGGGAAGAG 964  
Qy 121 TCGATGGACAGATTTGGAAGACTTAGCCGGTCAAGGAACCTTGGGGATCACTGCGGAGG 180  
Db 965 TCGATGGACAGATTTGGAAGACTTAGCCGGTCAAGGAACCTTGGGGATCACTGCGGAGG 1024  
Qy 181 ACTCATCAAGAAAGTCCGGGATTTGTTGATCATAGTGGGATCAAGCAAACTCGAGAT 240  
Db 1025 ACTCATCAAGAAAGTCCGGGATTTGTTGATCATAGTGGGATCAAGCAAACTCGAGAT 1084  
Qy 241 ATGGCTCGCCTTGGAAAGGGAATCTCCGGCCCTGGGATTCGAGGATCCGAAGTTGTACGTAT 300  
Db 1085 ATGGCTCGCCTTGGAAAGGGAATCTCCGGCCCTGGGATTCGAGGATCCGAAGTTGTACGTAT 1144  
Qy 301 GGAAGACTTACAGGCTTGGATTTATATCTTTTCATAGGAACCTACTGCAAGGGTAAG 360  
Db 1145 GGAAGACTTACAGGCTTGGATTTATATCTTTTCATAGGAACCTACTGCAAGGGTAAG 1204  
Qy 361 CTTCAGAGACACAGTGAAGTTCGCTTATCTCTCCACTCTTTCATGCGATATTTCAAC 420  
Db 1205 CTTCAGAGACACAGTGAAGTTCGCTTATCTCTCCACTCTTTCATGCGATATTTCAAC 1264  
Qy 421 GACTGGACACAGCTCGCTTTTGAAGCAAGTGACTTACTCTGGAATTTGATTTACACC 480  
Db 1265 GACTGGACACAGCTCGCTTTTGAAGCAAGTGACTTACTCTGGAATTTGATTTACACC 1324  
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Qy 541 CAGTTTCTTCTGCTCGGTTTCCACATTCCTCGATGACCTCTTGTATGTTCTTTGCGA 600  
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Qy 721 TTTCACAGAGGCTAAGACCAACAGAGGTCGCTTCGATGCGGATTTTGTGTT 780  
Db 1565 TTTCACAGAGGCTAAGACCAACAGAGGTCGCTTCGATGCGGATTTTGTGTT 1624  
Qy 781 TATTTTGAATTTCTTTTGTGATGACAGATTTTTCATGATATGCTCTCTGTCGTTTTTT 840  
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Db 1685 CTCTTCAAAACAGAGTGTCCGCTGTCAGTTCGTTCTCTTTCCTTCAACCAAACTTCAACTA 1744  
Qy 901 CAGACATCAATAACAGACATCTTACTTCGGTGTTCTCTCTTTTTTTTCCGAGAGTACAAG 960  
Db 1745 CAGACATCAATAACAGACATCTTACTTCGGTGTTCTCTCTTTTTTTTCCGAGAGTACAAG 1804  
Qy 961 ATGCAGATGACCTTCAAGCGATGCAAGCACTTCAGCTTGGAGGAGCAAGAGACCAAG 1020  
Db 1805 ATGCAGATGACCTTCAAGCGATGCAAGCACTTCAGCTTGGAGGAGCAAGAGACCAAG 1864  
Qy 1021 GGTTTCGCTTTTGTCCATATATTTCTGTTGTCACCTTATGTTCTTAACTACTTGTGTT 1080  
Db 1865 GGTTTCGCTTTTGTCCATATATTTCTGTTTCACTTCTTATGTTCTTAACTACTTGTGTT 1924  
Qy 1081 CTTTTCGTTGGATGTTGTTTCTATCGGTGGTGTCTTTCTTTTCTTTTGGATGATTCATC 1140

Db 1925 CTTTTTGGTTCGGATGTTGTTTCTATCGGTGGTGTCTTTCTTTCTTTGGAGCATATC 1984  
Qy 1141 ATTTATCGTGTGACATGTTTCTCTCTGCTGCTGTTTCTTTCTCTCTCTCTCTCTCTCTCT 1200  
Db 1985 ATTTATCGTGTGACATGTTTCTCTCTGCTGCTGTTTCTTTCTCTCTCTCTCTCTCTCT 2044  
Qy 1201 CAGGAGCCGCATCTCTTTCTAA 1223  
Db 2045 CAGGAGCCGCATCTCTTTCTAA 2067  
RESULT 3  
BD237787  
LOCUS  
DEFINITION Phaffiarhodozyma transforming vectors and transforming method  
ACCESSION BD237787  
VERSION BD237787.1 GI:33047557  
KEYWORDS JP 2002528124-A/2.  
SOURCE Xanthophyllomyces dendrorhous  
ORGANISM Xanthophyllomyces dendrorhous  
Eukaryota; Fungi; Basidiomycota; Hymenomycetes;  
Heterobasidiomycetes; Tremellomycetidae; Cystofilobasidiales;  
Cystofilobasidiaceae; Xanthophyllomyces.  
REFERENCE 1 (bases 1 to 350)  
AUTHORS Choi,E.S., Rhee,S.K., Sohn,J.H., Park,S.D., Lee,Y.H., Lee,S.J.,  
Jang,J.K., Choi,S.K. and Son,Y.R.  
TITLE Phaffiarhodozyma transforming vectors and transforming method  
JOURNAL Patent: JP 2002528124-A 2 03-SEP-2002;  
KOREA INSTITUTE OF SCIENCE AND TECHNOLOGY, HAITAI CONFECTIONERY CO  
LTD  
COMMENT OS Phaffia rhodozyma  
PN JP 2002528124-A/2  
PD 03-SEP-2002  
PP 29-MAY-1999 JP 2000579759  
PR 31-OCT-1998 KR 1998/46547  
PI EUI SUNG CHOI,SANG KI RHEE,JUNG HOON SOHN,SOO DONG PARK,YOON  
PI SEUNG JAE LEE, JAE KWEON JANG,SEOK KEUN CHOI,YOUNG ROK SON PC  
C12N15/09, C12N1/19/(C12N1/19, C12R1:645), C12N15/00 CC  
Phaffiarhodozyma transforming vectors and transforming method CC  
thereof  
FH Key Location/Qualifiers  
FT CDS Location/Qualifiers  
1..350  
/organism="Xanthophyllomyces dendrorhous"  
/mol\_type="genomic DNA"  
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ORIGIN  
Query Match 12.1%; Score 147.6; DB 6; Length 350;  
Best Local Similarity 97.4%; Pred. No. 1.6e-29;  
Matches 150; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
Qy 616 TCTGTAGTGACCCAGTACAGGAAGGAAAGGAGTCCATCTTCGCCAGGAAAGCCAGC 675  
Db 95 TCACAGGTGACCCAGTACAGGAAGGAAAGGAGTCCATCTTCGCCAGGAAAGCCAGC 154  
Qy 676 ATACGACCGAAAGCAGTCCGGTTACGGAGTTCAGACCAAGCCGCTTTTCCACAAGAGGC 735  
Db 155 ATACGACCGAAAGCAGTCCGGTTACGGAGTTCAGACCAAGCCGCTTTTCCACAAGAGGC 214  
Qy 736 TAGACCCACCAAGAGTTCGCTTCGATTGGCG 769  
Db 215 TAAGACCCACCAAGAGTTCGCTTCGATTGGAG 248  
RESULT 4  
CRU31912  
LOCUS  
DEFINITION Chlamydomonas reinhardtii ribosomal protein L41 (RPL41) mRNA,  
complete cds.  
336 bp mRNA linear PLN 17-SEP-1996

ACCESSION U1912  
VERSION U1912.1 GI:974301  
KEYWORDS  
SOURCE  
ORGANISM Chlamydomonas reinhardtii  
Chlamydomonas reinhardtii  
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;  
Chlamydomonadaceae; Chlamydomonas.  
REFERENCE 1 (bases 1 to 336)  
AUTHORS Stevens, D.R., Actea, A., Franzen, L.-G. and Purton, S.  
TITLE Direct Submission  
JOURNAL Submitted (20-JUL-1995) Saul Purton, Biology, University College  
London, Wer Street, London WC1E 6BT, UK  
FEATURES  
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/db\_xref="taxon:3055"  
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CDS 12..311  
/gene="RPL41"  
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/protein\_id="AAB08435.1"  
/db\_xref="GI:974302"  
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## ORIGIN

Query Match 9.4%; Score 115; DB 8; Length 336;  
Best Local Similarity 83.9%; Pred. No. 1.7e-20;  
Matches 130; Conservative 0; Mismatches 25; Indels 0; Gaps 0;  
Qy 612 TGTCTCTAGTGTAGCCAGTACAGAGGAAAGGACTCCATCTTCGCCAGGAAAGC 671  
Db 67 TGATGATGAAGTACACCCAGTACAGACTGGCAGGCTCTCTTACCGCAGGCGAAGC 126  
Qy 672 GACGATACGACCGAAGCAGTCGGTTACGAGGTGACACCAAGCCGCTTTCCACAAGA 731  
Db 127 GCCGCTACGACCGCAGCAGTCGGTTACGAGGTGACACCAAGCCGCTTTCCACAAGA 186  
Qy 732 AGGCTAAGACCCAGAGAGTCTGCTTCGATTG 766  
Db 187 AGGCCAAGACCAACCAAGAGATCGTGTGCGCATG 221

## RESULT 5

CR382128\_05  
WPCOMMENT  
Sequence split into 31 fragments LOCUS CR382128 Accession CR382128

Fragment Name	Begin	End
CR382128_00	1	110000
CR382128_01	100001	210000
CR382128_02	200001	310000
CR382128_03	300001	410000
CR382128_04	400001	510000
CR382128_05	500001	610000
CR382128_06	600001	710000
CR382128_07	700001	810000
CR382128_08	800001	910000
CR382128_09	900001	1010000
CR382128_10	1000001	1110000
CR382128_11	1100001	1210000
CR382128_12	1200001	1310000
CR382128_13	1300001	1410000
CR382128_14	1400001	1510000
CR382128_15	1500001	1610000
CR382128_16	1600001	1710000
CR382128_17	1700001	1810000

CR382128\_18 1800001 1910000  
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CR382128\_26 2600001 2710000  
CR382128\_27 2700001 2810000  
CR382128\_28 2800001 2910000  
CR382128\_29 2900001 3010000  
CR382128\_30 3000001 3066374  
Continuation (6 of 31) of CR382128 from base 500001 (CR382128 Yarrowia lipolytica chromosome)  
Query Match 9.3%; Score 113.8; DB 8; Length 110000;  
Best Local Similarity 85.2%; Pred. No. 5.3e-20;  
Matches 127; Conservative 0; Mismatches 22; Indels 0; Gaps 0;  
Qy 621 AGGTGACCCAGTACAAAGAGGAAAGGACTTCCATCTTCGCCAGGAAAGCGCATACG 680  
Db 61442 AGGTGACCCAGTACAAAGGCGGTAAAGCTTCTCTGACGTCAGGGTAAGCGCATACG 61501  
Qy 681 ACCGAAAGCAGTCCGTTACGAGGTACAGCCAGCCGCTTTTCCACAAGAGGCTAAGA 740  
Db 61502 ACCGAAAGCAGTCCGTTACGAGGTACAGCCAGCAGATTTTCCACAAGAGGCGCAAGA 61561  
Qy 741 CCACCAAGAGGTGCTCTTCGATTGCGGCTGCG 769  
Db 61562 CCACCAAGAGGTGCTCTTCGACTCGAG 61590  
RESULT 6  
AR382552 AR382552 688 bp DNA linear PAT 18-DEC-2003  
LOCUS Sequence 38 from patent US 6610514.  
ACCESSION AR382552  
VERSION AR382552.1 GI:40091283  
KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 688)  
AUTHORS Kondo, K. and Miura, Y.  
TITLE Yeast vector and method of producing proteins using the same  
JOURNAL Patent: US 6610514-A 38 26-AUG-2003;  
FEATURES  
source Location/Qualifiers  
1..688  
/organism="unknown"  
/mol\_type="genomic DNA"

## ORIGIN

Query Match 8.8%; Score 107.8; DB 6; Length 688;  
Best Local Similarity 79.9%; Pred. No. 1.8e-18;  
Matches 127; Conservative 0; Mismatches 32; Indels 0; Gaps 0;  
Qy 621 AGGTGACCCAGTACAAAGAGGAAAGGACTTCCATCTTCGCCAGGAAAGCGCATACG 680  
Db 438 AGGTGACCCAGTACAAAGGCTGTTAAAGCTTCCCTTTTCCAGGGTAAGCGTGTATG 497  
Qy 681 ACCGAAAGCAGTCCGTTACGAGGTACAGCCAGCCGCTTTTCCACAAGAGGCTAAGA 740  
Db 498 ACCGTAAGCAATCCGTTACGTTGTCAGGTCAGCAAGCAGATTTTCCACAAGAGGCTAAGA 557  
Qy 741 CCACCAAGAGGTGCTCTTCGATTGCGGCTGATTGTTGT 779  
Db 558 CCACCAAGAGGTGTTTGGGTTGAGTGTGTGCT 596

## RESULT 7

YSRPGL41 YSRPGL41 1048 bp DNA linear PLN 06-NOV-2001  
LOCUS  
DEFINITION Pichia guilliermondii PGL41 gene for ribosomal protein L41, partial

```

cds.
D10153
VERSION D10153.1 GI:218561
SOURCE Pichia guilliermondii
ORGANISM Pichia guilliermondii
REFERENCE Eukaryote; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
AUTHORS Saccharomycetales; Saccharomycetaceae; Pichia.
JOURNAL 1 (bases 1 to 1048)
COMMENT Kawai,S.
These data kindly submitted in computer readable form by: Shinya
Kawai
Dept. Agricultural Chemistry
The University of Tokyo
Bunkyo-ku, Tokyo 113
Japan
Phone: 03-3812-2111 x3087
Fax: 03-3812-9246.
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Best Local Similarity 70.0%; Pred.No.1.8e-18;
Matches 145; Conservative 0; Mismatches 62; Indels 0; Gaps 0;
QY 561 TTCCACATTCCTCGATGACCTCCTTGATGTTCTTTGCGAACGTTTCTGTTCTGTCTGT 620
DB 749 TTCCAAAGACCAGAGAACCTACTGCAAGGTAAGACTGCCGTAAGCACACCAACACA 808
QY 621 AGGTGACCCAGTACAAGAAGGAAAGACATCCATCTTTGCGCCAGGGAAGCGACGATACG 680
DB 809 AGGTGACCCAAATACAAGCGAGGTAAAGCCCTCTTTGTTGCGCCAGGTAAGAGATATG 868
QY 681 ACCGAAGCAGTCGCGTTACGAGGTACAGACCAAGCCGTTTCCACAAAGAGCTAAGA 740
DB 869 ACCGTAAGCAATCCGGTTTCGGTGGTCAAAACCAAGCCCGTTTTTCCAAAGAAAGCCAAGA 928
QY 741 CCACCAAGAGGTGCGTCTCTTCGATTGG 767
DB 929 CTACCAAGAGGTTGTGTTGAGATTGG 955
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/mol_type="unassigned DNA"

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Query Match      8.8%; Score 107.8; DB 6; Length 2086;
Best Local Similarity 79.9%; Pred. No. 1.9e-18;
Matches 127; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

Qy 621 AGGTGACCCAGTACAGAAGGAAAGGACTCCATCTTCGCCAGGAAAGCGACGATACG 680
    |||||
Db 1548 AGGTTACCCAGTACAGAAGGCTGGTAAGCTTCCCTCTTTCGCCAGGTAAGCGTGTATG 1607

Qy 681 ACCGAAAGCAGTCGGGTTACGAGGTACAGCAAGCCCGGTTTCCACAAGAGGCTAAGA 740
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Db 1608 ACCGTAAGCAATCCGTTACGGTGGTCAACCAAGCCAGTTTCCACAAAAGGCTAAAA 1667

Qy 741 CCACAGAAGAGTGGTCTTCGATTGGCGGTATTTTGT 779
    |||||
Db 1668 CCACAGAAGAGTGTGTTTGGGTTGGAGTGTGTGTCT 1706

RESULT 10
LOCUS      E11620
DEFINITION Candida utilis L41 gene.
ACCESSION E11620
VERSION    E11620.1 GI:22025256
KEYWORDS   JP 1996173170-A/4.
SOURCE     Pichia jadinii
ORGANISM   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
REFERENCE  1 (bases 1 to 2086)
AUTHORS    Misawa,N., Kondo,K. and Kajiwara,S.
TITLE      TRANSFORMATION SYSTEM OF CANDIDA UTILIS YEAST AND EXPRESSION OF
JOURNAL    HETEROLOGOUS GENE THEREWITH
COMMENT     Patent: JP 1996173170-A 4 09-JUL-1996;
            KIRIN BREWERY CO LTD
            OS Candida utilis
            PN JP 1996173170-A/4
            PD 09-JUL-1996
            PF 28-APR-1995 JP 1995129287
            PR 25-MAY-1994 JP 94P 135015, 26-OCT-1994 JP 94P 285823 PI
            MISAWA NORIHIKO, KONDO KEIJI, KAJIWARA SUSUMU PC
            C12N15/09,C07H21/04,C12N1/19,(C12N1/19,C12R1/72); CC
            strandedness: Double;
            CC topology: Linear;
            FH Key Location/Qualifiers
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            FT CDS join(1111..1114,1482..1798)
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            FT mutation replace(1644,'a')
            FT /phenotype='cycloheximide resistant'.
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ORIGIN
Query Match      8.8%; Score 107.8; DB 6; Length 2086;
Best Local Similarity 79.9%; Pred. No. 1.9e-18;
Matches 127; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

Qy 621 AGGTGACCCAGTACAGAAGGAAAGGACTCCATCTTCGCCAGGAAAGCGACGATACG 680
    |||||
Db 1548 AGGTTACCCAGTACAGAAGGCTGGTAAGCTTCCCTCTTTCGCCAGGTAAGCGTGTATG 1607

Qy 681 ACCGAAAGCAGTCGGGTTACGAGGTACAGCAAGCCCGGTTTCCACAAGAGGCTAAGA 740
    |||||
Db 1608 ACCGTAAGCAATCCGTTACGGTGGTCAACCAAGCCAGTTTCCACAAAAGGCTAAAA 1667

Qy 741 CCACAGAAGAGTGGTCTTCGATTGGCGGTATTTTGT 779
    |||||
Db 1668 CCACAGAAGAGTGTGTTTGGGTTGGAGTGTGTGTCT 1706


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Db 1608 ACCGTAAGCAATCCGTTACGGTGGTCAACCAAGCCAGTTTCCACAAAAGGCTAAAA 1667
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Qy 741 CCACAGAAGAGTGGTCTTCGATTGGCGGTATTTTGT 779
    |||||
Db 1668 CCACAGAAGAGTGTGTTTGGGTTGGAGTGTGTGTCT 1706

RESULT 11
LOCUS      AR382551
DEFINITION Sequence 37 from patent US 6610514.
ACCESSION AR382551
VERSION    AR382551.1 GI:40091282
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 2086)
AUTHORS    Kondo,K. and Miura,Y.
TITLE      Yeast vector and method of producing proteins using the same
JOURNAL    Patent: US 6610514-A 37 26-AUG-2003;
FEATURES   Location/Qualifiers
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ORIGIN
Query Match      8.8%; Score 107.8; DB 6; Length 2086;
Best Local Similarity 79.9%; Pred. No. 1.9e-18;
Matches 127; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

Qy 621 AGGTGACCCAGTACAGAAGGAAAGGACTCCATCTTCGCCAGGAAAGCGACGATACG 680
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Db 1548 AGGTTACCCAGTACAGAAGGCTGGTAAGCTTCCCTCTTTCGCCAGGTAAGCGTGTATG 1607

Qy 681 ACCGAAAGCAGTCGGGTTACGAGGTACAGCAAGCCCGGTTTCCACAAGAGGCTAAGA 740
    |||||
Db 1608 ACCGTAAGCAATCCGTTACGGTGGTCAACCAAGCCAGTTTCCACAAAAGGCTAAAA 1667

Qy 741 CCACAGAAGAGTGGTCTTCGATTGGCGGTATTTTGT 779
    |||||
Db 1668 CCACAGAAGAGTGTGTTTGGGTTGGAGTGTGTGTCT 1706

RESULT 12
LOCUS      YSARPL41
DEFINITION Candida utilis DNA for ribosomal protein L41, complete cds.
ACCESSION D67040
VERSION    D67040.1 GI:1255905
KEYWORDS   ribosomal protein L41.
SOURCE     Pichia jadinii
ORGANISM   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
REFERENCE  1 (sites)
AUTHORS    Kondo,K., Saito,T., Kajiwara,S., Takagi,M. and Misawa,N.
TITLE      A transformation system for the yeast Candida utilis: use of a
            modified endogenous ribosomal protein gene as a drug-resistant
            marker and ribosomal DNA as an integration target for vector DNA
            J. Bacteriol. 177 (24), 7171-7177 (1995)
            96099302
            PUBMED 8522525
            REFERENCE 2 (bases 1 to 2086)
            AUTHORS    Kondo,K.
            JOURNAL    Unpublished
            REFERENCE 3 (bases 1 to 2086)
            AUTHORS    Kondo,K.
            TITLE      Direct Submission
            JOURNAL    Submitted (26-SEP-1995) Keiji Kondo, Central Laboratories for Key
            Technology, KIRIN BREWERY CO., LTD.; 1-13-5 Fukuura, Kanazawa-ku,
            Yokohama, Kanagawa 236, Japan (Tel:045-788-7218, Fax:045-788-4042)

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FEATURES source Location/Qualifiers  
1..2086 /organism="Pichia jadinii"  
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CDS  
exon  
intron  
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ORIGIN  
Query Match 8.8%; Score 107.8; DB 8; Length 2086;  
Best Local Similarity 79.9%; Pred. No. 1.9e-18;  
Matches 127; Conservative 0; Mismatches 32; Indels 0; Gaps 0;  
621 AGGTGACCCAGTACAGGAGGAAGGACTCCATCTTCGCCAGGGAAGCGATACG 680  
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1608 ACCGTAGCAATCCGTTACGTTACGGTGTCAACCAAGCCAGTGTTCACAAAAGGCTTAAA 1667  
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741 CCACCAAGAAGTCGTCCTTCGATTGGCGGTATTGTTGT 779  
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1668 CCACCAAGAAGTGTGTTTGGGTTTGGAGTGTGTTGCT 1706  
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RESULT 13  
RIC340 444 bp mRNA linear PLN 02-FEB-1999  
LOCUS Rice mRNA for ribosomal protein L41 (340 gene), partial sequence.  
DEFINITION  
ACCESSION D10406  
VERSION D10406.1 GI:218112  
KEYWORDS ribosomal protein L41.  
SOURCE  
ORGANISM  
Oryza sativa  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
1 (sites)  
Uchimiya,H., Kidou,S., Shimazaki,T., Aotsuka,S., Takamatsu,S.,  
Nishi,R., Hashimoto,H., Matsubayashi,Y., Kidou,N., Umeda,M. and  
Kato,A.  
Random sequencing of cDNA libraries reveals a variety of expressed  
genes in cultured cells of rice (Oryza sativa L.)  
Plant J. 2, 1005-1009 (1992)  
2 (bases 1 to 444)  
Kidou,S., Umeda,M., Kato,A. and Uchimiya,H.  
Plant cDNA homologue to rat insulinoma gene encoding ribosomal  
protein S15  
Nucleic Acids Res. 21 (8), 2013 (1993)  
JOURNAL 93261842  
MEDLINE  
PUBMED 8493114  
REFERENCE 3 (bases 1 to 444)  
Uchimiya,H.  
Direct Submission  
Submitted (27-JAN-1992) Hirofumi Uchimiya, Institute of Mol. &  
Cell. Bioscience, The University of Tokyo, Department of Cellular  
Function, 1-1-1 Yayoi, Bunkyo-ku, Tokyo 113, Japan  
(E-mail:huchimiya@tansei.ac.u-tokyo.ac.jp)  
Tel:03-3812-2111(ex.7844), Fax:03-3812-2910)  
Submitted (27-Jan-1992) to DDBJ by:  
Hirofumi Uchimiya  
Institute of Applied Microbiology

University of Tokyo  
Bunkyo-ku, Tokyo 113  
Japan  
Phone: 03-3812-2111 x7844  
Fax: 03-3812-291.  
Location/Qualifiers  
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/db\_xref="taxon:4530"  
/tissue\_type="callus"

FEATURES source  
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Best Local Similarity 82.1%; Pred. No. 2.9e-17;  
Matches 119; Conservative 0; Mismatches 26; Indels 0; Gaps 0;  
615 TTCGTAGTGCACCCAGTACAGGAGGAAGGACTCCATCTTCGCCAGGGAAGCGAC 674  
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110 TTCAAAGGTCACCTCAGTACAGGAGGTAAGGACAGCCTGTCTGCCAGGGAAGCGCC 169  
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675 GATACGACCGAAGCAGTCGCGTTACGAGGTACAGCAAGCCGTTTTCACAGAAGG 734  
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170 GTTATGACCGTACGATCAGGATATGTTGTCAGCAAGCCCTGTTTTCACAGAAGG 229  
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735 CTATGACCCACCAAGAGGTCGTCTCT 759  
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230 CAAAACCCACCAAGAGTGTGTCT 254  
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RESULT 14.  
AK058924 676 bp mRNA linear PLN 24-JUL-2003  
LOCUS Oryza sativa (japonica cultivar-group) cDNA clone:001-009-C01, full  
insert sequence.  
ACCESSION AK058924  
VERSION AK058924.1 GI:32968942  
KEYWORDS FLI cDNA; oligo-capping.  
SOURCE  
ORGANISM  
Oryza sativa (japonica cultivar-group)  
Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
1  
The Rice Full-length cDNA Consortium, National Institute of  
Agrobiological Sciences Rice Full-length cDNA Project Team,  
Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K.,  
Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Hotta,I.,  
Kojima,K., Namiki,T., Ohneda,E., Yahagi,W., Suzuki,K., Li,C.,  
Ohtsuki,K., Shishiki,T., Foundation of Advancement of International  
Science Genome Sequencing & Analysis Group, Ootomo,Y., Murakami,K.,  
Iida,Y., Sugano,S., Fujimura,T., Suzuki,Y., Tsunoda,Y.,  
Kuroaki,T., Kodama,T., Masuda,H., Kobayashi,M., Xie,Q., Lu,M.,  
Nariawa,R., Sugiyama,A., Mizuno,K., Yokomizo,S., Niihara,J.,  
Ikeda,R., Ishibiki,J., Kawamata,M., Yoshimura,A., Miura,J.,  
Kusumegi,T., Oka,M., Ryu,R., Ueda,M., Matsubara,K., RIKEN,  
Kawai,J., Carninci,P., Adachi,J., Aizawa,K., Arakawa,T., Fukuda,S.,  
Hara,A., Hashidume,W., Hayatsu,N., Imotani,K., Ishii,Y., Itoh,M.,  
Kagawa,I., Kondo,S., Konno,H., Miyazaki,A., Otsu,N., Ota,Y.,  
Saito,R., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T.,  
Yoshino,M. and Hayashizaki,Y.  
Collection, mapping, and annotation of over 28,000 cDNA clones from  
japonica rice  
Science 301 (5631), 376-379 (2003)  
JOURNAL 22752273  
MEDLINE  
PUBMED 12869764  
REFERENCE 2 (bases 1 to 676)  
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Doi,K.,  
Fujimura,T., Fukuda,S., Hanagaki,T., Hara,A., Hashizume,W.,  
Hayashida,K., Hayashizaki,Y., Hayatsu,N., Hiramoto,K., Hirooka,T.,  
Hori,F., Hotta,I., Iida,J., Iida,Y., Ikeda,R., Imamura,K.,  
Imotani,K., Ishibiki,J., Ishii,Y., Ishikawa,M., Itoh,M., Kagawa,I.,  
Kanagawa,S., Katoh,H., Kawagashira,N., Kawai,J., Kawamata,M.,

Kikuchi, S., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M., Kodama, T., Kojima, K., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Kurosaki, T., Kusumegi, T., Li, C., Lu, M., Masuda, H., Matsubara, K., Matsuyama, T., Miura, J., Miyazaki, A., Mizuno, K., Murakami, K., Murata, M., Nagata, T., Nakamura, M., Namiki, T., Nariakawa, R., Niikura, J., Nishi, K., Nomura, K., Numasaki, R., Ohneda, E., Ohno, M., Ohtsuki, K., Oka, M., Ooka, H., Oota, N., Ota, Y., Otomo, Y., Ryu, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Satoh, K., Shibata, K., Shinagawa, A., Shiraki, T., Shishiki, T., Sogabe, Y., Sugano, S., Sugiyama, A., Suzuki, K., Suzuki, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Tsunoda, Y., Ueda, M., Waki, K., Xie, Q., Yahagi, W., Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and Yoshimura, A.

**TITLE** Direct Submission  
**JOURNAL** Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail: skikuchi@nias.affrc.go.jp)  
 Tel: 81-29-838-7007, Fax: 81-29-838-7007  
 This clone is one of the 28K full-length cDNA clones from japonica rice.

**COMMENT** URL : <http://cdna01.dna.affrc.go.jp/cdna/>  
 NIAS Rice Full-length cDNA Project Team: Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T., and Yamamoto, M.

FATS Genome Sequencing & Analysis Group: Otomo, Y., Iida, Y., Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M., Kodama, T., Kurosaki, T., Kusumegi, T., Lu, M., Masuda, H., Miura, J., Mizuno, K., Nariakawa, R., Niikura, J., Oka, M., Ryu, R., Sugano, S., Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S., Yoshimura, A., Matsubara, K. and Murakami, K.

Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hara, A., Hashizume, W., Hayashida, K., Ikeda, R., Iida, J., Imamura, K., Imoto, K., Ishii, Y., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J., Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koyama, S., Kurihara, C., Matsuyama, T., Miyazaki, R., Ohno, M., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ooka, M., Oota, N., Ota, Y., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Satoh, K., Shibata, K., Shinagawa, A., Shiraki, T., Shishiki, T., Sogabe, Y., Sugano, S., Sugiyama, A., Suzuki, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Tanaka, T., Tomaru, A., Toya, T., Waki, K., Yasunishi, A. and Hayashizaki, Y.

**FEATURES** Location/Qualifiers  
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**ORIGIN**  
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 Best Local Similarity 82.1%; Pred. No. 2.9e-17;  
 Matches 119; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

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 Db 36 TTCACAAAGTCTACTCGTACAAAGAGGTTAGGACAGCTGTCTGCCAGGGAAGCGCC 95  
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 QY 675 GATACGACCGAAAGCAGTCCGGTTAGCGAGGTTCAGACCAAGCCGTTTTCACAAAGAGG 734  
 |||||  
 Db 96 GTTATGACCGTGAAGCAGTTCAGGATATGGTGGTCAGACCAAGCTGTCTTCACAAAGAGG 155  
 |||||  
 QY 735 CTAAGACCAACCAAGAGAGTTCGCTCT 759  
 |||||  
 Db 156 CAAAACCAACCAAGAGAGTTGTGCT 180  
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# **RESULT 15** **AK069083** **LOCUS** **DEFINITION**

AK069083  
 Oryza sativa (japonica cultivar-group) cDNA clone: J023009C02, full insert sequence.  
 AK069083  
 AK069083.1 GI:32979107  
 FLI\_CDNA; CAP trapper.  
 Oryza sativa (japonica cultivar-group)  
 Oryza sativa (japonica cultivar-group)  
 Eukaryota; Viridiplantae; Streptophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

## **REFERENCE** **AUTHORS**

The Rice Full-length cDNA Consortium, National Institute of Agrobiological Sciences Rice Full-length cDNA Project Team: Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group: Otomo, Y., Murakami, K., Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y., Kurosaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M., Nariakawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Niikura, J., Ikeda, R., Ishibiki, J., Kawamata, M., Yoshimura, A., Miura, J., Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., RIKEN, Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Hayatsu, N., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kondo, S., Konno, H., Miyazaki, A., Osato, N., Ota, Y., Saito, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Yoshino, M. and Hayashizaki, Y.

## **TITLE**

Japonica rice  
 Science 301 (5631), 376-379 (2003)  
 22752273  
 12869764

## **JOURNAL** **MEDLINE** **PUBMED**

2 (bases 1 to 2173)  
 Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K., Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayashizaki, Y., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Hotta, I., Iida, J., Iida, Y., Ikeda, R., Imamura, K., Imoto, K., Ishibiki, J., Ishii, Y., Ishikawa, M., Itoh, M., Kagawa, I., Motani, K., Nishi, K., Nishikawa, N., Kawai, J., Kawamata, M., Kikuchi, S., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M., Kodama, T., Kojima, K., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Kurosaki, T., Kusumegi, T., Li, C., Lu, M., Masuda, H., Matsubara, K., Matsuyama, T., Miura, J., Miyazaki, A., Mizuno, K., Murakami, K., Murata, M., Nagata, T., Nakamura, M., Namiki, T., Nariakawa, R., Niikura, J., Nishi, K., Nomura, K., Ooka, H., Oota, N., Ota, Y., Otomo, Y., Ryu, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Satoh, K., Shibata, K., Shinagawa, A., Shiraki, T., Shishiki, T., Sogabe, Y., Sugano, S., Sugiyama, A., Suzuki, K., Suzuki, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Tsunoda, Y., Ueda, M., Waki, K., Xie, Q., Yahagi, W., Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and Yoshimura, A.

## **Direct Submission** **Submitted (05-DEC-2001)**

Shoshi Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail: skikuchi@nias.affrc.go.jp)  
 Tel: 81-29-838-7007, Fax: 81-29-838-7007

## **TITLE** **JOURNAL**

This clone is one of the 28K full-length cDNA clones from japonica rice.  
 URL : <http://cdna01.dna.affrc.go.jp/cdna/>  
 NIAS Rice Full-length cDNA Project Team: Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T. and

Yamamoto, M.

**source**

1. 2173

### Query Match

Query Match 8.5%: Score 103.4: DB 8: Length 2173:

Search completed: January

17:05:CT, 15007, 04 5-



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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 18, 2005, 08:40:39 ; Search time 739.931 Seconds  
(without alignments)  
8676.543 Million cell updates/sec

Title: US-09-830-691A-1  
Perfect score: 1223  
Sequence: 1 atgttcacattcccaagac.....gagccgcatctcttttctaa 1223

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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5: Geneseq2001bs.\*  
6: Geneseq2002as.\*  
7: Geneseq2002bs.\*  
8: Geneseq2003as.\*  
9: Geneseq2003bs.\*  
10: Geneseq2003cs.\*  
11: Geneseq2003ds.\*  
12: Geneseq2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1223	100.0	1223	3	AA15567 Phaffia r
2	1213.4	99.2	2192	3	AA15580 Phaffia r
3	147.6	12.1	347	3	AA15568 Phaffia r
4	119.8	9.8	467	10	ADC76428 DNA homol
5	119.8	9.8	467	10	ADK59686 Plant DNA
6	119.4	9.8	495	3	Aaf07944 Fusarium
7	112.2	9.2	513	3	AA11322 Aspergill
8	110.6	9.0	519	10	ADC75158 T harzian
9	110.6	9.0	659	10	ADK56011 Plant DNA
10	110.6	9.0	669	10	ADC75810 DNA homol
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12	107.8	8.8	2086	2	AAT08602 Ribosomal
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20	103.2	8.4	333	8	ABZ55708 Aspergill
21	102	8.3	420	10	ADC75809 DNA homol

22	102	8.3	420	10	ADK59683	Adk59683 Plant DNA
23	101	8.3	388	12	ADO57260	Ado57260 DNA encod
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25	100.6	8.2	577	3	AAC39588	Aac39588 Zea may
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28	98.2	8.0	1333	4	AAH29831	Aah29831 S cerevis
29	97.6	8.0	276	6	ABL74526	Ab174526 Corn tass
30	97.6	8.0	315	12	ADJ44315	Adj44315 Plant cDN
31	97.6	8.0	491	3	AAC38359	Aac38359 Zea may
32	96.6	7.9	1262	4	AAH29778	Aah29778 S cerevis
33	95	7.8	321	2	AAQ36738	Aaq36738 Sequence
34	95	7.8	2842	2	AAQ36739	Aaq36739 Sequence
c 35	94.6	7.7	395	6	ABK63114	ABK63114 Rat sequ
c 36	94.6	7.7	395	10	ADBS1806	Adbs1806 Primay r
37	94.2	7.7	491	10	ADC75159	Adc75159 T harzian
38	94.2	7.7	536	12	ADJ42888	Adj42888 Plant cDN
39	93.6	7.7	625	10	ADC76435	Adc76435 DNA homol
40	93.6	7.7	625	10	ADK59688	Adk59688 Plant DNA
41	93.6	7.7	633	10	ADK56014	Adk56014 Plant DNA
42	93.2	7.6	324	10	ADC75808	Adc75808 DNA homol
43	93.2	7.6	324	10	ADK56006	Adk56006 Plant DNA
c 44	93.2	7.6	423	10	ABX61264	Abx61264 Arabidops
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ALIGNMENTS

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ID AA15567 standard; DNA; 1223 BP.  
XX  
AC AA15567;  
XX  
DT 15-SEP-2003 (revised)  
DT 25-SEP-2000 (first entry)  
XX  
DE Phaffia rhodozyma L41 gene.  
XX  
KW Astatanthin; L41; yeast; carotenoid; cyclohexamide-resistance;  
KW site-directed mutagenesis; selectable marker; ribosomal DNA; ds.  
XX Xanthophyllomyces dendrorhous.  
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W0200026387-A1.

11-MAY-2000.

29-MAY-1999; 99WO-KR000265.

31-OCT-1998; 98KR-00046547.

(KOAD ) KOREA ADV INST SCI & TECHNOLOGY.  
(HAIT-) HAI TAI CONFECTIONERY CO LTD.

Choi E, Rhee S, Sohn J, Park S, Lee YH, Lee SJ, Jang JK;  
Choi SK, Son YR;

WPI; 2000-365630/31.  
P-PSDB; AAY94261.

Novel vector comprising a cyclohexamide-resistance gene and a ribosomal  
DNA useful for the transformation of Phaffia rhodozyma.

Claim 2; Page 35-36; 43pp; English.

The present genomic sequence is the L41 gene encoding a Phaffia rhodozyma  
ribosomal protein. The present sequence is the wild-type sequence, with a  
proline residue at position 56. This residue is responsible for P.  
rhodozyma sensitivity to cyclohexamide. However, when this residue is  
mutated via site-directed mutagenesis to give rise to a glutamine at  
position 56, the yeast gains resistance to cyclohexamide. The modified  
L41 gene can be used as a selectable marker of a transforming vector for  
P. rhodozyma. The vector can be used to carry foreign DNA, e.g. the  
astaxanthin gene, a carotenoid. A Phaffia rhodozyma rDNA gene can also be  
included in the vector to enhance the intergration efficiency of foreign  
DNA into host genomes. (Updated on 15-SEP-2003 to standardise OS field)

Sequence 1223 BP; 291 A; 286 C; 265 G; 381 T; 0 U; 0 Other;

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Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 CAATATATCCAGTGCATCGAAGAGTTTGTGGATAAACCAGACAGTTTCAAGGGAAGAG 120  
QY 121 TCGATGGACAGATTGGGAAGATTAGCCGGTCAAGAACTTGGGGATCACGTGGCGGAGG 180  
DB 121 TCGATGGACAGATTGGGAAGATTAGCCGGTCAAGAACTTGGGGATCACGTGGCGGAGG 180  
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DB 481 TGTATTTAGCCCTCACAGGTACATATCATATCTCCACCCACCCCTGCCCAACTTCTT 540  
QY 541 CAGTTTCATCTGCTCTCGGTTTCCACATTCCTGTAGTACCTCTTGTATGTTCTTTGCGA 600  
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DB 841 CTCTTCAACAGAGTCTCGCTCGAGTTCGTTCTTCTTCCAAACCAAACTTCAACTA 900  
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RESULT 2  
AAA15580  
ID AAA15580 standard; DNA; 2192 BP.

XX AC AAA15580;  
 XX DT 15-SEP-2003 (revised)  
 XX DT 25-SEP-2000 (first entry)  
 XX DE Phaffia rhodozyma L41 gene.  
 XX KW Ataxanthin; L41; yeast; carotenoid; cyclohexamide-resistance;  
 XX KW site-directed mutagenesis; selectable protein; ribosomal DNA; ds.  
 XX OS Xanthophyllomyces dendrorhous.  
 XX PH Key Location/Qualifiers  
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 FT FT TATA\_signal 155..158  
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 FT FT /\*tag= e  
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 FT FT exon 1044..1080  
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 FT FT intron 1081..1193  
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 FT FT /number= 5  
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 FT FT /number= 7  
 XX WO200026387-A1.  
 XX PN 11-MAY-2000.  
 XX PD 29-MAY-1999; 99WO-KR000265.  
 XX PP 31-OCT-1998; 98KR-00046547.  
 XX PR (KROAD ) KOREA ADV INST SCI & TECHNOLOGY.  
 XX PA (HAIT-) HAI TAI CONFECTIONERY CO LTD.  
 XX

PI Choi E, Rhee S, Sohn J, Park S, Lee YH, Lee SJ, Jang JK;  
 PI Choi SK, Son YR;  
 XX WPI; 2000-365630/31.  
 DR P-PSDB; AAY94261.  
 XX Novel vector comprising a cyclohexamide-resistance gene and a ribosomal  
 FT DNA useful for the transformation of Phaffia rhodozyma.  
 XX Disclosure; Fig 1; 43pp; English.  
 CC The present genomic sequence is the L41 gene encoding a Phaffia rhodozyma  
 CC ribosomal protein. The present sequence is the wild-type sequence, with a  
 CC proline residue at position 56. This residue is responsible for P.  
 CC rhodozyma sensitivity to cyclohexamide. However, when this residue is  
 CC mutated via site-directed mutagenesis to give rise to a glutamine at  
 CC position 56, the yeast gains resistance to cyclohexamide. The modified  
 CC L41 gene can be used as a selectable marker of a transforming vector for  
 CC P. rhodozyma. The vector can be used to carry foreign DNA, e.g. the  
 CC astaxanthin gene, a carotenoid. A Phaffia rhodozyma rDNA gene can also be  
 CC included in the vector to enhance the integration efficiency of foreign  
 CC DNA into host genomes. (Updated on 15-SEP-2003 to standardise OS field)  
 XX Sequence 2192 BP; 539 A; 518 C; 443 G; 692 T; 0 U; 0 Other;  
 SQ Query Match 99.2%; Score 1213.4; DB 3; Length 2192;  
 Best Local Similarity 99.5%; Pred. No. 0;  
 Matches 1217; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
 QY 1 ATGGTCAAGCTTCCCAAGACTCGACGTGAGTTATAGCAATTTCAACAACCTCTCAGACGA 60  
 DB 705 ATGGTCAAGCTTCCCAAGACTCGACGTGAGTTATAGCAATTTCAACAACCTCTCAGACGA 764  
 QY 61 CAAATATTCAGTGCATCGAAGAGTTTGTGGATAAACGCGACAGTTTCAAGGGAAGAG 120  
 DB 765 CAAATATTCAGTGCATCGAAGAGTTTGTGGATAAACGCGACAGTTTCAAGGGAAGAG 824  
 QY 121 TCGATGACAGATTTCGGAAGACTTAGCCGGTCAAGGAACCTGGGGATCAGTGGCGAGG 180  
 DB 825 TCGATGACAGATTTCGGAAGACTTAGCCGGTCAAGGAACCTGGGGATCAGTGGCGAGG 884  
 QY 181 ACTCATCAGAAGAGTCGGGATTTGTTGATCATAGTGGATCAAGACAACTGGAGGAT 240  
 DB 885 ACTCATCAGAAGAGTCGGGATTTGTTGATCATAGTGGATCAAGACAACTGGAGGAT 944  
 QY 241 ATGGCTCGCTTGGGAAGGAATCTCGGCTGGATTTCGAGGATCCGAAAGTTCTAGGTAT 300  
 DB 945 ATGGCTCGCTTGGGAAGGAATCTCGGCTGGATTTCGAGGATCCGAAAGTTCTAGGTAT 1004  
 QY 301 GGAAAGCTTACACGGCTTGGATTATTTATTTATAGGAACCTACTGCAAGGGTAAGG 360  
 DB 1005 GGAAAGCTTACACGGCTTGGATTATTTATTTATAGGAACCTACTGCAAGGGTAAGG 1064  
 QY 361 CTTGCAAGAGCACACGTAAGTCGTTATCTCTCTCACTCTTTTCATGGCATATGTCAAC 420  
 DB 1065 CTTGCAAGAGCACACGTAAGTCGTTATCTCTCTCACTCTTTTCATGGCATATGTCAAC 1124  
 QY 421 GACTGGACAACGCTCCGTTTGGAAACAAGTCAGCTTACCTGTGAATTTGATTCTACAC 480  
 DB 1125 GACTGGACAACGCTCCGTTTGGAAACAAGTCAGCTTACCTGTGAATTTGATTCTACAC 1184  
 QY 481 TGTATTTAGCCCTTCAACAGGTACATATCATCTCTCCACCCACCCTGCCCAACTTCTT 540  
 DB 1185 TGTATTTAGCCCTTCAACAGGTACATATCATCTCTCCACCCACCCTGCCCAACTTCTT 1244  
 QY 541 CAGTTTCATCTTGCTCTCGGTTTCCACATTTCCCTGATGACCTCTCTGTATGTTCTTGGCA 600  
 DB 1245 CAGTTTCATCTTGCTCTCGGTTTCCACATTTCCCTGATGACCTCTCTGTATGTTCTTGGCA 1304  
 QY 601 ACGTTTGTGTTTCTGTTCTGTAGTGACCCAGTACAGAGGGAAGGACTCCACTCTTCGC 660  
 DB 1305 ACGTTTGTGTTTCTGTTCTGTAGTGACCCAGTACAGAGGGAAGGACTCCACTCTTCGC 1364

Qy	661	CCAGGGAAGCGACGATACGACCGAAAGCAGTCCGGTTACGGAGGTGACAGCAAGCCCGT	720
Db	1365	CCAGGGAAGCGACGATACGACCGAAAGCAGTCCGGTTACGGAGGTGACAGCAAGCCCGT	1424
Qy	721	TTTCCACAAGAGGCTAAGACCAACCAAGAAGTTCGTTTCGATTCGGCGGTATTTTGT	780
Db	1425	TTTTTCACAAGAGGCTAAGACCAACCAAGAAGTTCGTTTCGATTCGGGTACGTTTTTGT	1484
Qy	781	TATTTTGAATTCCTTTTGTCTATGTCAGACATTTTGTGATGATTATGCTCCTCTGTGCTTTTT	840
Db	1485	TATTTTGAATTCCTTTTGTGATGTCAGACATTTTGTGATGATTATGCTCCTCTGTGCTTTTT	1544
Qy	841	CTCTTCAAAACAGAGTGCTCCGTCGCGATGCGTTCCTTCCTTCCAAACAAACCTTCAACTA	900
Db	1545	CTCTTCAAAACAGAGTGCTCCGTCGCGATGCGTTCCTTCCTTCCAAACAAACCTTCAACTA	1604
Qy	901	CAGACATCATAAACAGACATCTTACTTCGSGTGTCTCTCTTTTTTCCGACAGTACAAG	960
Db	1605	CAGACATCATAAACAGACATCTTACTTCGSGTGTCTCTCTTTTTTCCGACAGTACAAG	1664
Qy	961	ATGCAGATGACCTTCAAGCGATGCAAGCACTTCGAGCTTCGAGGAGACAAGAAGCAAG	1020
Db	1665	ATGCAGATGACCTTCAAGCGATGCAAGCACTTCGAGCTTCGAGGAGACAAGAAGCAAG	1724
Qy	1021	GGTTCGCTTTTGTGCCATAATCTCTGGTTCACCTCTTATGTCTTAAACGTACTGTGT	1080
Db	1725	GGTTCGCTTTTGTGCCATAATCTCTGGTTCACCTCTTATGTCTTAAACGTACTGTGT	1784
Qy	1081	CCTTTTTGGTTTCGAGATGTTTCTATTCGSGTGTCTTTCTTTTTCGATGCAATTATC	1140
Db	1785	CCTTTTTGGTTTCGAGATGTTTCTATTCGSGTGTCTTTCTTTTTCGATGCAATTATC	1844
Qy	1141	ATTTTATCGTGTTCGACTGTTTTCTCTGCTCGTTTCTTCTCTCTGACTGTGCTTCT	1200
Db	1845	ATTTTATCGTGTTCGACTGTTTTCTCTGCTCGTTTCTTCTCTCTGACTGTGCTTCT	1904
Qy	1201	CAGGAGCGCCATCTCTTCTTCAA	1223
Db	1905	CAGGAGCGCCATCTCTTCTTCAA	1927

RESULT 3	
AAA15568	
ID	AAA15568 standard; cDNA; 347 BP.
XX	
AC	AAA15568;
XX	
DT	15-SEP-2003 (revised)
DT	25-SEP-2000 (first entry)
XX	
DE	Phaffia rhodozyma I41 cDNA.

XX Astaxanthin; L41; yeast; carotenoid; cyclohexamide-resistance;  
KW site-directed mutagenesis; selectable marker; ribosomal DNA; ss.  
XX Xanthochyllumvires dendrorhous.  
OS

XX	Key	Location/Qualifiers
FH	CDS	30..350
FT		/tag= a
FT		/product= "L41 protein"

XX PN WO200026387-A1.

11-MAY-2000.

XX 29-MAY-1999: 99WO-KR000265.

XX  
PP 31-OCT-1998. 98KPB-00046547.

XX  
PA (KOAD ) KOREA ADV INST SCI & TECHNOLOGY.  
PA (HAIT-) HAI TAI CONFECTIONERY CO LTD.

PI	Choi E, Rhee S, Sohn J, Park S, Lee YH, Lee SJ, Jang JK;
PP	Choi SK, Son YR;
XX	WPI; 2000-365630/31.
XX	P-PSDB; AAY94261.
DR	
DR	
XX	
XX	Novel vector comprising a cyclohexamide-resistance gene and a ribosomal
PT	DNA useful for the transformation of <i>Phaffia rhodozyma</i> .
PT	
XX	
XX	Claim 3; Page 36-37; 43pp; English.
XX	
XX	The present cDNA sequence is the L41 gene encoding a <i>Phaffia rhodozyma</i>
CC	ribosomal protein. The present sequence is the wild-type sequence, with a
CC	proline residue at position 56. This residue is responsible for P.
CC	<i>rhodozyma</i> sensitivity to cyclohexamide. However, when this residue is
CC	mutated via site-directed mutagenesis to give rise to a glutamine at
CC	position 56, the yeast gains resistance to cyclohexamide. The modified
CC	L41 gene can be used as a selectable marker of a transforming vector for
CC	<i>P. rhodozyma</i> . The vector can be used to carry foreign DNA, e.g. the
CC	ataxanthin gene, a carotenoid. A <i>Phaffia rhodozyma</i> rDNA gene can also be
CC	included in the vector to enhance the integration efficiency of foreign
CC	DNA into host genomes. (Updated on 15-SEP-2003 to standardise OS field)
XX	
XX	Sequence 347 BP; 103 A; 98 C; 87 G; 59 T; 0 U; 0 Other;
XX	

	Query Match	12.1%;	Score 147.6;	DB.3;	Length 347;
	Best Local Similarity	97.4%;	Pred. No. 6.7e-33;		
	Matches 150;	Conservative	0;	Mismatches 4;	Indels 0; Gaps 0
Qy	616	TCGTGAGGTGACCCAGTACAAAGAGGGGAAAGGACTTCCATCTTCGCCCCAGGAGAAAGCGACG	675		
Db	95	TCAACAGGTGACCCAGTACAAAGAGGGGAAAGGACTTCCATCTTCGCCCCAGGAGAAAGCGACG	154		
Qy	676	ATACGACCCAAAGACGTCGGGTTCACGAGGTCAGACCAAGCCGGTTTTTCACAAGAAGGC	735		
Db	155	ATACGACCCAAAGACGTCGGGTTCACGAGGTCAGACCAAGCCGGTTTTTCACAAGAAGGC	214		
Qy	736	TAAGACCAACCAAGAGGTGTCCTTCGATTGGCG	769		
Db	215	TAAGACCAACCAAGAGGTGTCCTTCGATTGGAG	248		

RESULT 4  
ADC76428  
ID ADC76428 standard: DNA: 467 BP.

XX ADC76428;

XX  
DT 01-JAN-2004 (first entry)

XX DNA homologous to phytopathogen resistance-related cDNA - SEQ ID 1697;  
DE  
XX rice; yeast; poppy; plant; disease resistance; anti-fungal;  
KW phytonathogen; gene shuffling; ds.  
KW

XX Unidentified.

XX PN WO2003020905-A2.

XX  
PD  
13-MAR-2003XX  
PF 30-AUG-2002: 2002WO-US027883.XX  
21-MVC-2001-2001US-0316392P-XX  
P3  
(DOWNS) TOW THEM CO[illegible]

XX 2003 200105/20

xx Novel isolated nucleic acid derived from *Nicotiana benthamiana*, *Oryzae*  
pt  
20  
21  
22 *Gaelectromyces cerevisiae*, *Trichoderma harzianum* and *Papaver*  
23

PT rheas, useful for conferring disease resistance in plants.

PS Claim 1; SEQ ID NO 1697; 617pp; English.

XX The invention relates to a novel isolated nucleic acid derived from  
CC Nicotiana benthamiana, Oryza sativa (rice), Saccharomyces cerevisiae  
CC (yeast), Trichoderma harzianum (Hypocrea lixi) and Papaver rhoeas  
CC (poppy) and a sequence that hybridises to them under conditions of low  
CC stringency, where expression of the nucleic acid in a plant results in a  
CC disease resistance phenotype. The polynucleotides of the invention  
CC demonstrate anti-fungal activity and may be useful in conferring disease  
CC resistance in a plant against phytopathogen such as Aspergillus flavus,  
CC Gibberella fujikuroi and Gibberella zeae. Furthermore, the  
CC polynucleotides may be useful to retrieve unknown sequences and in gene  
CC shuffling or sexual PCR procedures. The current sequence is that of the  
CC DNA of the invention which is homologous to that of the phytopathogen  
CC resistance-related contig cDNAs.

XX Sequence 467 BP; 119 A; 134 C; 126 G; 88 T; 0 U; 0 Other;

Query Match 9.8%; Score 119.8; DB 10; Length 467;  
Best Local Similarity 88.4%; Pred. No. 7.7e-24;  
Matches 130; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

Qy 621 AGGTGACCCAGTACAGAGGGAAGGACTCCATCTTCGCCAGGGAAGCGAGTACG 680  
Db 107 AGGTGACCCAGTACAGAGGCTGGCAAGGCTCCCTCTTCGCCAGGGAAGCGTTCACG 166  
Qy 681 ACCGAAGAGCGTCCGGTTACGGGTGTCAGACCAAGCCGCTTCCACAGAAGGCTAAGA 740  
Db 167 ACCGTAAGCAGTCCGGTTACGGGTGTCAGACCAAGCCGCTTCCACAGAAGGCTAAGA 226  
Qy 741 CCACCAAGAAGGTCGTCCTTCGATTGG 767  
Db 227 CCACCAAGAAGGTCGTCCTTCAGATTAG 253

# RESULT 5

ADKS9686  
ID. ADKS9686 standard; DNA; 467 BP.

XX ADKS9686;

XX 06-MAY-2004 (first entry)

DE Plant DNA sequence which confers altered metabolic characteristic #7069.

XX altered metabolic characteristic; plant; acid metabolism;  
KW alcohol metabolism; fatty acid metabolism;  
KW branched fatty acid metabolism; alkaloid metabolism;  
KW amino acid metabolism; ester metabolism; glyceride metabolism;  
KW phenolic metabolism; carbohydrate metabolism; sterol metabolism;  
KW terpene metabolism; isoprenoid metabolism; alkene metabolism;  
KW alkyne metabolism; hydrocarbon metabolism; ketone metabolism;  
KW quinone metabolism; disease resistance; gene shuffling; sexual PCR; de.

XX Unidentified.

XX WO2003020936-A1.

XX 13-MAR-2003.

XX 30-AUG-2002; 2002WO-US027884.

XX 31-AUG-2001; 2001US-0316471P.

XX (DOWC) DOW CHEM CO.

XX (DOWC) DOW AGROSCIENCES LLC.

XX Weglarz T, Gachotte D, Blakeslee B, McCreary DA, Pell RJ;

XX Oriedo JVB, Croseley R, Reddy AS, Shukla V, Larrinua I, Miller BA;

XX WPI; 2003-313091/30.

XX

PT Novel genes that confer altered metabolic characteristics in Nicotiana  
PT benthamiana plants, useful for altering the levels of metabolites e.g.  
PT acids, fatty acids, amino acids, carbohydrates, hydrocarbons and sterols.

PS Claim 1; SEQ ID NO 7069; 2576pp; English.

XX The invention comprises DNA sequences which confer an altered metabolic  
CC characteristic when they are expressed in a plant. The DNA sequences of  
CC the invention are useful for producing plants with an altered metabolic  
CC characteristic, such as: altered acid metabolism, alcohol metabolism,  
CC fatty acid metabolism, branched fatty acid metabolism, alkaloid or other  
CC base metabolism, altered amino acid metabolism, altered ester metabolism,  
CC altered glyceride metabolism, altered phenolic metabolism, altered  
CC carbohydrate metabolism, altered sterol, oxygenated terpene, or  
CC isoprenoid metabolism, alkene or alkyne metabolism, hydrocarbon  
CC metabolism, ketone or quinone metabolism. The DNA sequences of the  
CC invention may be used to provide disease resistance in a plant and gene  
CC shuffling or sexual PCR procedures. The present nucleic acid represents a  
CC DNA sequence of the invention.

XX Sequence 467 BP; 119 A; 134 C; 126 G; 88 T; 0 U; 0 Other;

Query Match 9.8%; Score 119.8; DB 10; Length 467;  
Best Local Similarity 88.4%; Pred. No. 7.7e-24;  
Matches 130; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

Qy 621 AGGTGACCCAGTACAGAGGGAAGGACTCCATCTTCGCCAGGGAAGCGAGTACG 680  
Db 107 AGGTGACCCAGTACAGAGGCTGGCAAGGCTCCCTCTTCGCCAGGGAAGCGTTCACG 166  
Qy 681 ACCGAAGAGCGTCCGGTTACGGGTGTCAGACCAAGCCGCTTCCACAGAAGGCTAAGA 740  
Db 167 ACCGTAAGCAGTCCGGTTACGGGTGTCAGACCAAGCCGCTTCCACAGAAGGCTAAGA 226  
Qy 741 CCACCAAGAAGGTCGTCCTTCGATTGG 767  
Db 227 CCACCAAGAAGGTCGTCCTTCAGATTAG 253

# RESULT 6

AAF07944

ID AAF07944 standard; cDNA; 495 BP.

XX AAF07944;

XX 13-MAR-2001 (first entry)

XX Fusarium venenatum EST SEQ ID NO:467.

XX Multiple gene expression; filamentous fungal cell; EST;

XX expressed sequence tag; Fusarium venenatum; Aspergillus niger;

XX Aspergillus oryzae; Trichoderma reesei; identification; recombination;

XX culture condition; environmental stress; spore morphogenesis;

XX metabolic pathway engineering; catabolic pathway engineering; ss.

XX Fusarium venenatum.

XX WO200056762-A2.

XX 28-SEP-2000.

XX 22-MAR-2000; 2000WO-US007781.

XX 22-MAR-1999; 99US-00273623.

XX (NOVO) NOVO NORDISK BIOTECH INC.

XX (NOVO) NOVO NORDISK AS.

XX Berka RM, Rey MW, Shuster JR, Kauppinen S, Clausen IG, Olsen PB;

XX WPI; 2000-594572/56.

XX

PT Monitoring differential expression of genes in filamentous fungal cells  
PT uses fluorescence-labeled nucleic acids isolated from the cells and a  
PT substrate of expressed sequence tags.

XX Claim 86; Page 564; 3161pp; English.

XX The present invention describes a method for monitoring differential  
XX expression of genes in a first filamentous fungal (FF) cell relative to  
XX expression of the same genes in one or more second filamentous fungal  
XX cells. The method uses fluorescence-labeled nucleic acids isolated from  
XX the FF cells and a substrate of expressed sequence tags (EST). The ESTs  
XX are used in the methods for monitoring differential expression of genes  
XX in a first filamentous fungal (FF) cell relative to expression of the  
XX same genes in one or more second filamentous fungal cells. Monitoring the  
XX global expression of genes from FF cells allows the production potential  
XX of the microorganisms to be improved. New genes may be discovered.  
XX possible functions of unknown open reading frames can be identified and  
XX gene copy number variation and stability can be monitored. The expression  
XX of genes can be used to study how FF cells adapt to changes in culture  
XX conditions, environmental stress, spore morphogenesis, recombination,  
XX metabolic or catabolic pathway engineering. Using ESTs provides several  
XX advantages over genomic or random cDNA clones including elimination of  
XX redundancy as one spot on an array equals one gene or open reading frame,  
XX and organisation of the microarrays based on function of the gene  
XX products to facilitate analysis of the results. AAF07478 to AAF11247  
XX represents ESTs from Fusarium venenatum; AAF11248 to AAF11853 represents  
XX ESTs from Aspergillus niger; AAF11854 to AAF14878 represents ESTs from  
XX Aspergillus oryzae; and AAF14879 to AAF15337 represents ESTs from  
XX Trichoderma reesei, which are all specifically claimed in the present  
XX invention

SQ Sequence 495 BP; 132 A; 120 C; 119 G; 107 T; 0 U; 17 Other;

Query Match 9.8%; Score 119.4; DB 3; Length 495;  
Best Local Similarity 86.6%; Pred. No. 1e-23; Indels 0; Gaps 0;  
Matches 129; Conservative 0; Mismatches 20;

QY 621 AGGTGACCCAGTACAAAGAGGAAAGGACTCCATCTTCGCCAGGAGGAAAGCGATACG 680  
DB 80 AGGTGACCCAGTACAAAGGCTGGAAGGCTCCCTGTTGCCAGGAAAGCGTCNATATG 139  
QY 681 ACCGAAAGCAGTCGCGTTACGAGGTTCAGACCAAGCCGTTTTCACAAAGGCTAAGA 740  
DB 140 ACCGCAANACAGTCCCGTTATGTTGTTGTCAGACCAANCCGTTCTCCACAAAGGCCAAGA 199  
QY 741 CCACCAAGAGGTGCTCTTCGATTGGCG 769  
DB 200 CCACCAAGAGGTGCTCTTCGATTGGAG 228

RESULT 7  
AAFL1322  
ID AAF11322 standard; cDNA; 513 BP.

AC AAF11322;

DT 13-MAR-2001 (first entry)

DE Aspergillus niger EST SEQ ID NO:3845.

XX Multiple gene expression; filamentous fungal cell; EST;  
KW expressed sequence tag; Fusarium venenatum; Aspergillus niger;  
KW Aspergillus oryzae; Trichoderma reesei; identification; recombination;  
KW culture condition; environmental stress; spore morphogenesis;  
KW metabolic pathway engineering; catabolic pathway engineering; ss.

OS Aspergillus niger.

XX WO200056762-A2.

XX 28-SEP-2000.

XX 22-MAR-2000; 2000WO-US007781.

XX 22-MAR-1999; 99US-00273623.

XX (NOVO ) NOVO NORDISK BIOTECH INC.

XX (NOVO ) NOVO NORDISK AS.

XX Berka RM, Rey MW, Shuster JR, Kauppinen S, Clausen IG, Olsen PB;

XX WPI; 2000-594572/56.

XX Monitoring differential expression of genes in filamentous fungal cells  
XX uses fluorescence-labeled nucleic acids isolated from the cells and a  
XX substrate of expressed sequence tags.

XX Claim 87; Page 1720; 3161pp; English.

XX The present invention describes a method for monitoring differential  
XX expression of genes in a first filamentous fungal (FF) cell relative to  
XX expression of the same genes in one or more second filamentous fungal  
XX cells. The method uses fluorescence-labeled nucleic acids isolated from  
XX the FF cells and a substrate of expressed sequence tags (EST). The ESTs  
XX are used in the methods for monitoring differential expression of genes  
XX in a first filamentous fungal (FF) cell relative to expression of the  
XX same genes in one or more second filamentous fungal cells. Monitoring the  
XX global expression of genes from FF cells allows the production potential  
XX of the microorganisms to be improved. New genes may be discovered.  
XX possible functions of unknown open reading frames can be identified and  
XX gene copy number variation and stability can be monitored. The expression  
XX of genes can be used to study how FF cells adapt to changes in culture  
XX conditions, environmental stress, spore morphogenesis, recombination,  
XX metabolic or catabolic pathway engineering. Using ESTs provides several  
XX advantages over genomic or random cDNA clones including elimination of  
XX redundancy as one spot on an array equals one gene or open reading frame,  
XX and organisation of the microarrays based on function of the gene  
XX products to facilitate analysis of the results. AAF07478 to AAF11247  
XX represents ESTs from Fusarium venenatum; AAF11248 to AAF11853 represents  
XX ESTs from Aspergillus niger; AAF11854 to AAF14878 represents ESTs from  
XX Aspergillus oryzae; and AAF14879 to AAF15337 represents ESTs from  
XX Trichoderma reesei, which are all specifically claimed in the present  
XX invention

SQ Sequence 513 BP; 141 A; 128 C; 133 G; 110 T; 0 U; 1 Other;

Query Match 9.2%; Score 112.2; DB 3; Length 513;  
Best Local Similarity 84.6%; Pred. No. 1.2e-21;  
Matches 126; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 621 AGGTGACCCAGTACAAAGAGGAAAGGACTCCATCTTCGCCAGGAGGAAAGCGATACG 680  
DB 98 AGGTGACCCAGTACAAAGGCTGGAAGGCTCCCTGTTGCCAGGGAAGCGTTCGTTACG 157  
QY 681 ACCGAAAGCAGTCGCGTTACGAGGTTCAGACCAAGCCGTTTTCACAAAGGCTAAGA 740  
DB 158 ACCGGAAGCAGAGCGGTTATGTTGTTGTCAGACCAAGCCGCTTCTCCACAAAGGCCAAGA 217  
QY 741 CCACCAAGAGGTGCTCTTCGATTGGCG 769  
DB 218 CCACCAAGAGGTGCTCTTCGTTTGAG 246

RESULT 8  
ADC75158  
ID ADC75158 standard; cDNA; 519 BP.

AC ADC75158;

XX 01-JAN-2004 (first entry)

XX T harzianum phytopathogen resistance-related contig cDNA - SEQ ID 82.  
DE rice; yeast; poppy; plant; disease resistance; anti-fungal;  
KW phytopathogen; gene shuffling; ss.



```
OS Hypocrea lixii.
XX WO2003020905-A2.
XX 13-MAR-2003.
XX 30-AUG-2002; 2002WO-US027883.
XX 31-AUG-2001; 2001US-0316392P.
XX (DOWC ) DOW CHEM CO.
XX Shukla V, Butler H, Larrinua I, Reddy AS;
XX WPI; 2003-290185/28.
XX Novel isolated nucleic acid derived from Nicotiana benthamiana, Oryzae
XX sativa, Saccharomyces cerevisiae, Trichoderma harzianum and Papaver
XX rhoeas, useful for conferring disease resistance in plants.
XX Claim 1; SEQ ID NO 82; 617pp; English.
XX The invention relates to a novel isolated nucleic acid derived from
XX Nicotiana benthamiana, Oryza sativa (rice), Saccharomyces cerevisiae
XX (yeast), Trichoderma harzianum (Hypocrea lixi) and Papaver rhoeas
XX (poppy) and a sequence that hybridises to them under conditions of low
XX stringency, where expression of the nucleic acid in a plant results in a
XX disease resistance phenotype. The polynucleotides of the invention
XX demonstrate anti-fungal activity and may be useful in conferring disease
XX resistance in a plant against phytopathogen such as Aspergillus flavus,
XX Gibberella fujikuroi and Gibberella zeae. Furthermore, the
XX polynucleotides may be useful to retrieve unknown sequences and in gene
XX shuffling or sexual PCR procedures. The current sequence is that of the
XX phytopathogen resistance-related contig cDNA of the invention.
XX Sequence 519 BP; 134 A; 131 C; 143 G; 110 T; 0 U; 1 Other;
XX
XX Query Match 9.0%; Score 110.6; DB 10; Length 519;
XX Best Local Similarity 83.9%; Pred. NO. 3.6e-21;
XX Matches 125; Conservative 0; Mismatches 24; Indels 0; Gaps 0;
XX
XX 621 AGGTGACCCAGTACAGAGGGAAGGACTCCATCTTCGCCAGGGAAGCGATACG 680
XX 127 AGGTCACTCAGTACAGGCGCGGAGGCTTCCCTGTTGCCCGGGAAGAGCGTTATG 186
XX 681 ACCGAAGCAGTCCGGTTACCGAGTCAAGCAAGCCCGTTTCCACAAGAGGCTAAGA 740
XX 187 ACCGAAGCAGGCGGTTATGGTGTAGACCAAGCCCGTCTTCCACAAGAGGCCAAGA 246
XX 741 CCACAAGAGGTCGTCTTCGATTGGCG 769
XX 247 CCACAAGAGGTCGTCTCGCGTTGGAG 275
XX
XX RESULT 9
XX ADK56011
XX ID ADK56011 standard; DNA; 659 BP.
XX AC ADK56011;
XX DT 06-MAY-2004 (first entry)
XX XX
XX Plant DNA sequence which confers altered metabolic characteristic #3394.
XX altered metabolic characteristic; plant; acid metabolism;
XX alcohol metabolism; fatty acid metabolism;
XX branched fatty acid metabolism; alkaloid metabolism;
XX amino acid metabolism; ester metabolism; glyceride metabolism;
XX phenolic metabolism; carbohydrate metabolism; sterol metabolism;
XX terpene metabolism; isoprenoid metabolism; alkene metabolism;
XX alkylne metabolism; hydrocarbon metabolism; ketone metabolism;
XX quinone metabolism; disease resistance; gene shuffling; sexual PCR; ds.
XX
XX OS Unidentified.
XX WO2003020936-A1.
XX 13-MAR-2003.
XX 30-AUG-2002; 2002WO-US027884.
XX 31-AUG-2001; 2001US-0316471P.
XX (DOWC ) DOW CHEM CO.
XX PA (DOWC ) DOW AGROSCIENCES LLC.
XX XX
XX Weglarz T, Gachotte D, Blakeslee B, McCreary DA, Pell RJ;
XX Oriedo JVB, Crosley R, Reddy AS, Shukla V, Larrinua I, Miller BA;
XX WPI; 2003-313091/30.
XX Novel genes that confer altered metabolic characteristics in Nicotiana
XX benthamiana plants, useful for altering the levels of metabolites e.g.
XX acids, fatty acids, amino acids, carbohydrates, hydrocarbons and sterols.
XX Claim 1; SEQ ID NO 3394; 2576pp; English.
XX The invention comprises DNA sequences which confer an altered metabolic
XX characteristic when they are expressed in a plant. The DNA sequences of
XX the invention are useful for producing plants with an altered metabolic
XX characteristic, such as: altered acid metabolism, alcohol metabolism,
XX fatty acid metabolism, branched fatty acid metabolism, alkaloid or other
XX base metabolism, altered amino acid metabolism, altered ester metabolism,
XX altered glyceride metabolism, altered phenolic metabolism, altered
XX carbohydrate metabolism, altered sterol, oxygenated terpene, or
XX isoprenoid metabolism, alkene or alkyne metabolism, hydrocarbon
XX metabolism, ketone or quinone metabolism. The DNA sequences of the
XX invention may be used to provide disease resistance in a plant and gene
XX shuffling or sexual PCR procedures. The present nucleic acid represents a
XX DNA sequence of the invention.
XX Sequence 659 BP; 174 A; 160 C; 177 G; 148 T; 0 U; 0 Other;
XX
XX Query Match 9.0%; Score 110.6; DB 10; Length 659;
XX Best Local Similarity 83.9%; Pred. NO. 4e-21;
XX Matches 125; Conservative 0; Mismatches 24; Indels 0; Gaps 0;
XX
XX 621 AGGTGACCCAGTACAGAGGGAAGGACTCCATCTTCGCCAGGGAAGCGATACG 680
XX 98 AGGTCACTCAGTACAGGCGCGGAGGCTTCCCTGTTGCCCGGGAAGAGCGTTATG 157
XX 681 ACCGAAGCAGTCCGGTTACCGAGTCAAGCAAGCCCGTTTCCACAAGAGGCTAAGA 740
XX 158 ACCGAAGCAGGCGGTTATGGTGTAGACCAAGCCCGTCTTCCACAAGAGGCCAAGA 217
XX 741 CCACAAGAGGTCGTCTTCGATTGGCG 769
XX 218 CCACAAGAGGTCGTCTCGCGTTGGAG 246
XX
XX RESULT 10
XX ADC75810
XX ID ADC75810 standard; DNA; 669 BP.
XX AC ADC75810;
XX DT 01-JAN-2004 (first entry)
XX XX
XX DNA homologous to phytopathogen resistance-related cDNA - SEQ ID 734.
XX rice; yeast; poppy; plant; disease resistance; anti-fungal;
XX phytopathogen; gene shuffling; ds.
XX Unidentified.
XX WO2003020905-A2.
XX
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XX PD 13-MAR-2003.
XX PF 30-AUG-2002; 2002WO-US027883.
XX PR 31-AUG-2001; 2001US-0316392P.
XX PA (DOWC ) DOW CHEM CO.
XX PI Shukla V, Butler H, Larrinua I, Reddy AS;
XX DR WPI; 2003-290185/28.
XX PT Novel isolated nucleic acid derived from Nicotiana benthamiana, Oryzae
XX PT sativa, Saccharomyces cerevisiae, Trichoderma harzianum and Papaver
XX PT rhoeas, useful for conferring disease resistance in plants.
XX PS Claim 1; SEQ ID NO 734; 617pp; English.
XX CC The invention relates to a novel isolated nucleic acid derived from
XX CC Nicotiana benthamiana, Oryza sativa (rice), Saccharomyces cerevisiae
XX CC (yeast), Trichoderma harzianum (Hypocrea lixii) and Papaver rhoeas
XX CC (poppy) and a sequence that hybridises to them under conditions of low
XX CC stringency, where expression of the nucleic acid in a plant results in a
XX CC disease resistance phenotype. The polynucleotides of the invention
XX CC demonstrate anti-fungal activity and may be useful in conferring disease
XX CC resistance in a plant against phytopathogen such as Aspergillus flavus,
XX CC Gibberella fujikuroi and Gibberella zeae. Furthermore, the
XX CC polynucleotides may be useful to retrieve unknown sequences and in gene
XX CC shuffling or sexual PCR procedures. The current sequence is that of the
XX CC DNA of the invention which is homologous to that of the phytopathogen
XX CC resistance-related contig cDNAs.
XX SQ Sequence 669 BP; 180 A; 163 C; 177 G; 149 T; 0 U; 0 Other;

Query Match 9.0%; Score 110.6; DB 10; Length 669;
Best Local Similarity 83.9%; Pred. No. 4e-21;
Matches 125; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

Qy 621 AGGTGACCCAGTACAGAGGGAAGGACTCCACTTCGCCAGGGAAGCGAGATACG 680
Db 108 AGGTCACTCAGTACAGAGCGCGGTTATGGTGTGTCAGACCAAGCCGCTCTCCACAGAGGCCAAGA 227

Qy 681 ACCGAAAGCAGTCCGGTTACGGAGGTGACAGCAAGCCCGTTTTCACAGAGGCTAAGA 740
Db 168 ACCGGAAGCAGAGCGGTTATGGTGTGTCAGACCAAGCCGCTCTCCACAGAGGCCAAGA 227

Qy 741 CCACCAAGAGGTGCTCTTCGATTGGCG 769
Db 228 CCACCAAGAGGTGCTCTCGGTTGGAG 256

RESULT 11
ADK59682
ID ADK59682 standard; DNA; 669 BP.
XX AC ADK59682;
XX DT 06-MAY-2004 (first entry)
XX DE Plant DNA sequence which confers altered metabolic characteristic #7065.
XX KW altered metabolic characteristic; plant; acid metabolism;
XX KW alcohol metabolism; fatty acid metabolism;
XX KW branched fatty acid metabolism; alkaloid metabolism;
XX KW amino acid metabolism; ester metabolism; glyceride metabolism;
XX KW phenolic metabolism; carbohydrate metabolism; steroid metabolism;
XX KW terpene metabolism; isoprenoid metabolism; alkene metabolism;
XX KW alkyne metabolism; hydrocarbon metabolism; ketone metabolism;
XX KW quinone metabolism; disease resistance; gene shuffling; sexual PCR; ds.
XX OS Unidentified.

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PN WO2003020936-A1.
XX PD 13-MAR-2003.
XX PF 30-AUG-2002; 2002WO-US027884.
XX PR 31-AUG-2001; 2001US-0316471P.
XX PA (DOWC ) DOW CHEM CO.
XX PI Weglarz T, Gachotte D, Blakeslee B, McCreary DA, Pell RJ;
XX DR Oriedo JVB, Crosley R, Reddy AS, Shukla V, Larrinua I, Miller BA;
XX PT WPI; 2003-313091/30.
XX PT Novel genes that confer altered metabolic characteristics in Nicotiana
XX PT benthamiana plants, useful for altering the levels of metabolites e.g.
XX PT acids, fatty acids, amino acids, carbohydrates, hydrocarbons and sterols.
XX PS Claim 1; SEQ ID NO 7065; 2576pp; English.
XX CC The invention comprises DNA sequences which confer an altered metabolic
XX CC characteristic when they are expressed in a plant. The DNA sequences of
XX CC the invention are useful for producing plants with an altered metabolic
XX CC characteristic, such as: altered acid metabolism, alcohol metabolism,
XX CC fatty acid metabolism, branched fatty acid metabolism, alkaloid or other
XX CC base metabolism, altered amino acid metabolism, altered ester metabolism,
XX CC altered glyceride metabolism, altered phenolic metabolism, altered
XX CC carbohydrate metabolism, altered steroid, oxygenated terpene, or
XX CC isoprenoid metabolism, alkene or alkyne metabolism, hydrocarbon
XX CC metabolism, ketone or quinone metabolism. The DNA sequences of the
XX CC invention may be useful to provide disease resistance in a plant and gene
XX CC shuffling or sexual PCR procedures. The present nucleic acid represents a
XX CC DNA sequence of the invention.
XX SQ Sequence 669 BP; 180 A; 163 C; 177 G; 149 T; 0 U; 0 Other;

Query Match 9.0%; Score 110.6; DB 10; Length 669;
Best Local Similarity 83.9%; Pred. No. 4e-21;
Matches 125; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

Qy 621 AGGTGACCCAGTACAGAGGGAAGGACTCCACTTCGCCAGGGAAGCGAGATACG 680
Db 108 AGGTCACTCAGTACAGAGCGCGGTTATGGTGTGTCAGACCAAGCCGCTCTTCACAGAGGCCAAGA 227

Qy 681 ACCGAAAGCAGTCCGGTTACGGAGGTGACAGCAAGCCCGTTTTCACAGAGGCTAAGA 740
Db 168 ACCGGAAGCAGAGCGGTTATGGTGTGTCAGACCAAGCCGCTCTTCACAGAGGCCAAGA 227

Qy 741 CCACCAAGAGGTGCTCTTCGATTGGCG 769
Db 228 CCACCAAGAGGTGCTCTCGGTTGGAG 256

RESULT 12
AAT08602
ID AAT08602 standard; DNA; 2086 BP.
XX AC AAT08602;
XX DT 16-OCT-2003 (revised)
XX DT 03-DEC-1996 (first entry)
XX DE Ribosomal protein L41 gene.
XX KW Ribosomal protein; expression vector; heterogene; yeast; GAP; PGK; PMA;
XX KW phosphoglyceric acid kinase; protoplasmic membrane proton ATPase;
XX KW glyceraldehyde-3-phosphoric acid dehydrogenase; resistance marker;
XX KW hygromycin B phosphotransferase; aminoglycoside-3'-phosphotransferase;
XX KW ss.
XX OS Pichia jadinii.

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XX FH Key Location/Qualifiers
XX exon 1111..1114
XX FT /*tag= a
XX FT /label= Exon 1.
XX FT intron 1115..1481
XX FT /*tag= b
XX FT /label= Intron 1.
XX FT exon 1482..1795
XX FT /*tag= c
XX FT /label= Exon 2.
XX PN W09532289-A1.
XX PD 30-NOV-1995.
XX PP 25-MAY-1995; 95WO-JP001005.
XX PR 25-MAY-1994; 94JP-00135015.
XX PR 26-OCT-1994; 94JP-00285823.
XX PR 28-APR-1995; 95JP-00129287.
XX PA (KIRI ) KIRIN BEER KK.
XX PI Kondo K, Kajiwara S, Misawa N;
XX WIPI; 1996-020584/02.
XX DR Ribosomal protein L41 gene, promoter and terminator sequences, isolated
XX PT from Candida utilis - used in vector for expression of hetero:gene(s) in
XX PT yeast.
XX Claim 4; Page 159-161; 252pp; Japanese.
XX PS The L41 ribosomal structural protein gene can be used in the construction
XX CC of expression vectors designed specifically to express heterogenes in
XX CC yeast. The vectors also comprise: a promoter and terminator sequence
XX CC selected from phosphoglyceric acid kinase (PGK), glyceraldehyde-3-
XX CC phosphoric acid dehydrogenase (GAP) and protoplasmic membrane proton
XX CC ATPase (PMA) genes isolated from Candida utilis; a drug resistance marker
XX CC selected from aminoglycoside-3'-phosphotransferase or hygromycin B
XX CC phosphotransferase; and the heterogene to be expressed. L41 confers
XX CC cyclohexamine resistance on the yeast. (Updated on 16-OCT-2003 to
XX CC standardise OS field)
XX SQ Sequence 2086 BP; 591 A; 458 C; 529 G; 508 T; 0 U; 0 Other;

Query Match 8.8%; Score 107.8; DB 2; Length 2086;
Best Local Similarity 79.9%; Pred. No. 4.2e-20;
Matches 127; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 621 AGGTGACCCAGTACAGAGGAAAGGACTCCATCTTCGCCAGGGAAGCGATACG 680
DB 1548 AGGTATCCAGTACAGAGGCTGGTAAGGCTTCCTCTTTGCCAGGTAAGCGTGTATG 1607

QY 681 ACCGAAAGCAGTCCGGTTACGGAGTCCAGCAAGCCCGTTTCCACAAGAGGCTAAGA 740
DB 1608 ACCGTAGCAATCCGGTTACGGTGGTCAACCAAGCCAGTTTCCACAAAAGGCTAAAA 1667

QY 741 CCACCAAGAGGTCGTCCTTCGATTCGGCGGTATTTTGT 779
DB 1668 CCACCAAGAGGTTGTTTTCGGTTTGGAGTGTGTGTCT 1706

RESULT 13
AAV31513
ID AAV31513 standard; DNA; 2086 BP.
XX AC AAV31513;
XX 17-OCT-2003 (revised)
DT 14-AUG-1998 (first entry)
XX

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DE Base sequence of DNA fragment containing L41 gene.
XX Candida utilis; yeast vector; promoter; marker gene; GAP gene;
XX high-efficiency integration; monellin; food; drug; L41; URA3; ss.
XX Pichia jadinii.
XX Key Location/Qualifiers
XX CDS 1111..1798
XX FT /*tag= a
XX FT /note= "contains intron"
XX FT intron 1117..1482
XX FT /*tag= b
XX FT /number= 1
XX FT /cons_splice= (5'site=yes, 3'site=no)
XX PN W09807873-A1.
XX PD 26-FEB-1998.
XX PP 22-AUG-1997; 97WO-JP002924.
XX PR 23-AUG-1996; 96JP-00241062.
XX PA (KIRI ) KIRIN BEER KK.
XX PI Kondo K, Miura Y;
XX WIPI; 1998-169177/15.
XX DR P-PSDB; AAW57490.
XX PT Yeast vector for multi-copying on to chromosomes of yeast such as Candida
XX PT utilis - contains a shortened promoter sequence linked to a marker gene
XX PT for high-efficiency integration.
XX Example; Fig 9; 107pp; Japanese.
XX This represents the base sequence of DNA fragment containing yeast L41
XX CC gene. This can be used in the construction of a yeast vector for multi-
XX CC copying on to chromosomes of yeast such as Candida utilis. The vector
XX CC contains a DNA homologous with a chromosomal gene of the yeast
XX CC (preferably ribosomal DNA (rDNA) such as the URA3, L41, PGK, GAP or PMA
XX CC gene), a marker gene to be used in transformant selection (such as a drug
XX CC resistance gene, e.g. the cycloheximide resistance gene L41, the G418
XX CC resistance gene Tn903-APT, or the hygromycin B resistance gene (from
XX CC E.coli) HPT), a shortened promoter sequence such as the C.utilis L41,
XX CC phosphoglycerate kinase (PGK), glyceraldehyde-3-phosphate dihydrogenase
XX CC (GAP) or plasma membrane proton ATPase (PMA) gene promoter and a gene of
XX CC interest from yeast or other origin. The vectors are useful in the
XX CC preparation of proteins for food or drug use in high efficiency. They can
XX CC be used especially for the production of single-chain monellin, which is
XX CC a low-calorie sweetener whose thermostability is greater than that of the
XX CC dimeric natural monellin. Multiple copies of the desired gene are
XX CC integrated into the yeast chromosome and high expression efficiency is
XX CC obtained. (Updated on 17-OCT-2003 to standardise OS field)
XX SQ Sequence 2086 BP; 591 A; 458 C; 529 G; 508 T; 0 U; 0 Other;

Query Match 8.8%; Score 107.8; DB 2; Length 2086;
Best Local Similarity 79.9%; Pred. No. 4.2e-20;
Matches 127; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 621 AGGTGACCCAGTACAGAGGAAAGGACTCCATCTTCGCCAGGGAAGCGATACG 680
DB 1548 AGGTATCCAGTACAGAGGCTGGTAAGGCTTCCTCTTTGCCAGGTAAGCGTGTATG 1607

QY 681 ACCGAAAGCAGTCCGGTTACGGAGTCCAGCAAGCCCGTTTCCACAAGAGGCTAAGA 740
DB 1608 ACCGTAGCAATCCGGTTACGGTGGTCAACCAAGCCAGTTTCCACAAAAGGCTAAAA 1667

QY 741 CCACCAAGAGGTCGTCCTTCGATTCGGCGGTATTTTGT 779
DB 1668 CCACCAAGAGGTTGTTTTCGGTTTGGAGTGTGTGTCT 1706

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RESULT 14
ADJ43725
ID ADJ43725 standard; cdna; 318 BP.
XX AC ADJ43725;
XX DT 06-MAY-2004 (first entry)
XX DE Plant cdna #4725.
XX KW Plant; gene; ss; transcription; plant genome augmentation; cereal;
KW soybean; alfalfa; sunflower; canola; cotton; peanut; tobacco; sugar beet;
KW maize; barley; sorghum; rice; wheat; crop plant; insecticide resistance;
KW stress tolerance; salt tolerance; cold tolerance; drought tolerance;
KW plant nutrition; apical dominance; dwarfism; early flowering; antiviral;
XX OS Eukaryota.
XX PN US2004016025-A1.
XX PD 22-JAN-2004.
XX PF 26-SEP-2002; 2002US-00260238.
XX PR 26-SEP-2001; 2001US-0325277P.
XX PR 26-SEP-2001; 2001US-0325448P.
XX PR 04-APR-2002; 2002US-0370620P.
XX PA (BUDWORTH) BUDWORTH P.
XX PA (MOUG/) MOUGHAMER T.
XX PA (BRIG/) BRIGGS S P.
XX PA (COOP/) COOPER B.
XX PA (GLAZ/) GLAZEBROOK J.
XX PA (GOFF/) GOFF S A.
XX PA (KATA/) KATAGIRI F.
XX PA (KREP/) KREPS J.
XX PA (PROV/) PROVART N.
XX PA (RICK/) RICHE D.
XX PA (ZHUT/) ZHU T.
XX PI Budworth P, Moughamer T, Briggs SP, Cooper B, Glazebrook J;
XX PI Goff SA, Katagiri F, Kreps J, Provart N, Ricke D, Zhu T;
XX DR WPI; 2004-190374/18.
XX PS New rice promoter, useful for manipulating crop plants to alter or
XX PT improve phenotypic characteristics, e.g. produce large quantities of oil
XX PT or proteins, resistance to insecticides, virus or fungi, stress tolerance
XX PT or high nutritional value.
XX PS Example 13; SEQ ID NO 4725; 230pp; English.
XX CC The invention relates to plant nucleotide sequences that direct seed-,
XX CC leaf- and/or stem-, panicle-, root- or pollen-specific or preferential
XX CC or constitutive transcription of an operatively linked nucleic acid
XX CC segment. The invention also relates to a method for augmenting a plant
XX CC genome and a method of identifying a gene, where its expression is
XX CC altered in the seed, leaf, stem, panicle, pollen, root or is constitutive
XX CC in a plant cell. The plant is a cereal, e.g. soybean, alfalfa, sunflower,
XX CC canola, cotton, peanut, tobacco or sugar beet, preferably maize, barley,
XX CC sorghum, rice or wheat. The polynucleotides and the polypeptides they
XX CC encode are useful for manipulating crop plants to alter or improve
XX CC phenotypic characteristics, to produce large quantities of oil or
XX CC proteins, to incur resistance to insecticides, viruses or fungi, and to
XX CC incur stress tolerance (e.g. salt, cold or drought) to ensure the plants
XX CC have a high nutritional value with reduced apical dominance or dwarfism,
XX CC early flowering or altered metabolic pathways. This sequence represents a
XX CC plant nucleic acid of the invention. Note: The sequence data for this
XX CC patent did not form part of the printed specification but was obtained in
XX CC electronic format directly from USPTO at seqdata.uspto.gov/sequence.html.

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XX SQ Sequence 318 BP; 103 A; 77 C; 83 G; 55 T; 0 U; 0 Other;
Query Match 8.5%; Score 104.2; DB 12; Length 318;
Best Local Similarity 81.2%; Pred. No. 2e-19;
Matches 121; Conservative 0; Mismatches 28; Indels 0; Gaps 0;
Oy 611 CTGTTTCTGTAGTGACCCAGTACAAAGAGGAAAGGACTCCATCTTTCGCCCGGAAAG 670
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 64 CTCCTTCACAAGGTCACCTCAGTACAAAGAGGTAAGCAGCAGCTGTCTGCCCGGAAAG 123
Oy 671 CGACGATACGACCGAAAGCGAGTCGCGTTACGGAGTCAGACCAAGCCCGTTTCCACAAG 730
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 124 CGCGTGTATGACCGTAAGCAGTCAGGATATGTTGTCAGACCAAGCCTGTTTCCACAAG 183
Oy 731 AAGGCTAAGACCCCAAGAGGTCGTCCT 759
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 184 AAGGCAAAACCCCAAGAGGATGTGCT 212
RESULT 15
ADJ43721
ID ADJ43721 standard; cdna; 315 BP.
XX AC ADJ43721;
XX DT 06-MAY-2004 (first entry)
XX DE Plant cdna #4721.
XX KW Plant; gene; ss; transcription; plant genome augmentation; cereal;
KW soybean; alfalfa; sunflower; canola; cotton; peanut; tobacco; sugar beet;
KW maize; barley; sorghum; rice; wheat; crop plant; insecticide resistance;
KW stress tolerance; salt tolerance; cold tolerance; drought tolerance;
KW plant nutrition; apical dominance; dwarfism; early flowering; antiviral;
XX OS Eukaryota.
XX PN US2004016025-A1.
XX PD 22-JAN-2004.
XX PF 26-SEP-2002; 2002US-00260238.
XX PR 26-SEP-2001; 2001US-0325277P.
XX PR 26-SEP-2001; 2001US-0325448P.
XX PR 04-APR-2002; 2002US-0370620P.
XX PA (BUDWORTH) BUDWORTH P.
XX PA (MOUG/) MOUGHAMER T.
XX PA (BRIG/) BRIGGS S P.
XX PA (COOP/) COOPER B.
XX PA (GLAZ/) GLAZEBROOK J.
XX PA (GOFF/) GOFF S A.
XX PA (KATA/) KATAGIRI F.
XX PA (KREP/) KREPS J.
XX PA (PROV/) PROVART N.
XX PA (RICK/) RICHE D.
XX PA (ZHUT/) ZHU T.
XX PI Budworth P, Moughamer T, Briggs SP, Cooper B, Glazebrook J;
XX PI Goff SA, Katagiri F, Kreps J, Provart N, Ricke D, Zhu T;
XX DR WPI; 2004-190374/18.
XX PS New rice promoter, useful for manipulating crop plants to alter or
XX PT improve phenotypic characteristics, e.g. produce large quantities of oil
XX PT or proteins, resistance to insecticides, virus or fungi, stress tolerance
XX PT or high nutritional value.
XX PS Example 13; SEQ ID NO 4721; 230pp; English.

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